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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacillus licheniformis
Bacillus licheniformis
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
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100.0%; Pred. No. 6.5e-279;
ive 0; Mismatches 0;
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Improved bacillus host cell
Patent: WO 03087148-A 1 23-OCT-2003;
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Sequence 1 from Patent WO03087148.
AX930045
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   AX437557
AE017327
AP006627_16
BA000004_13
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BA000028_20
CP000029_12
AE016748
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AL93528—
CP000033 03
AE015030—
SPNEU1908
AE07333
CQ788949
AR218808
BD003720
AX571760
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AX641669
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Best Local Similarity
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AUTHORS
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JOURNAL
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AX954657 Sequence
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Continuation (28 o
AX444675 Sequence
15896 Bacillus su
299118 Bacillus su
299118 Bacillus su
Continuation (26 o
Continuation (27 o
AX433201 Sequence
AE017012 Bacillus
Continuation (43 o
Continuation (43 o
AE017038 Bacillus
Continuation (43 o
                                                                                                                                                                                                                             ; Search time 5716 Seconds
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10491.575 Million cell updates/sec
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                                      GenCore (c) 1993
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                                                                                                                                                                                                                                    February 27, 2006,
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AE017327 Listeria
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tive 0; Mismatches 0;
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                    Unpublished
2 (bases 1 to 17787)
Bruschi, C. V.
Direct Submitseion
Submitted (11-DEC-1997) C.V. Bruschi, International Centre for Genetic Engineering and Biotechnology, Padriciano 99, I-34012
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bofC gene; csbX gene; nadA gene; nadC gene; nicotinate-nucleotide pyrophosphorylase; queA gene; quinolinate synthetase; ruvA gene; puruB gene; sporulation-specific protein; spovB gene; tRNA-quanine transglycosylase; yrbA gene; yrbB gene; yrbC gene; yrbD gene; yrbE gene; yrbC gene; bacillus subtilis
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                                         Bacillus licheniformis
Bacillus licheniformis
Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                  Length 459;
                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                     (DK)
                                                                                                                                Berka, R. and Clausen, I.G. Methods for monitoring multiple gene expression Patent: WO 0229113-A 3090 11-APR-2002; Novozymes Biotech, Inc. (US) ; Novozymes A/S (DE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AATTTGAACATGTCATTGAAGCCGTAAAATCATCCGGAA 459
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                                                                                                                                                                                                                                             1. .459
// Organism="Bacillus licheniformis"
// mol_type="unassigned DNA"
// db_xref="taxon:1402"
                                                                                                                                                                                                                                                                                                                                                                               tch
al Similarity 100.0%; Pred. No. 7.1e-115;
459; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                      Location/Qualifiers
  GI:21659483
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LITENGAMAVIDNSRQAVYGYDQRVEVFGTKGSAAADNSRPTTVEVSTADFVWKDKPH
                                                                                                                                                                                                                                                                                                                                                                                 FFFLERYKDSYEEEILRFAEAIGTNQETPCTGNDGLQAGRIARAAQQSLAFGMPVSIE
HTEKIAF"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGITITITICAGATIGATATAAAGCGGCTGGAAAGCCGGATGGCGGATGATCTGCGCAAAG
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69.0%; Pred. No. 3.2e-114;
tive 0; Mismatches 285; Indels
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/product="BofC protein"
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Winters, P., Wipat, A., Yamamoto, H., Yamane, K., Yasumoto, K., Yata, K., Yoshida, K., Yoshikawa, H.F., Zumstein, E., Yoshikawa, H. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      On Jul 7, 2003 this sequence version replaced gi:2635200. This entry contains data from release R16.1 of the Subtilist database. Further data on gene annotation and detailed information about changes from previous releases can be found at http://genolist.pasteur.fr/Subtilist/.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                        Submitted (27-JUN-2003) I. Moszer, A. Danchin, Institut Pasteur, Genetique des Genomes Bacteriens, 28 rue du Docteur Roux, 75724 Paris Cedex 15, FRANCE. E-mail: moszer@pasteur.fr, adanchin@pasteur.fr Phone: +33 (0)1 45 68 84 41, Fax: +33 (0)1 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Bacillus subtilis subsp. subtilis str. 168"
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                                                                                                                                                                                                                                                                                        Kunst, F., Ogasawara, N., Yoshikawa, H. and Danchin, A.
Direct Submission
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                                                                                                  10348 GAAAGAATGAGAGAGAGAGAGATATGTTAACTTTTCTATAAGACTTTGGCTGTTTTTA 10407
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                                                                                                                                                                                                                                                                                                                      701 GATTGATTATGTATCGCCCCAATATATTGTCATTGAAAACGGCGGGATCGGCTATCAGAT
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Bacteria; Firmicutes; Bacillales; Bacillaces, Bacillus.
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Z99118 AL009126
Z99118.2 GI:32468802
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HHPFTWPKBEDLEILETAPEDMKAQAYDLVLINGYELGGGSIRIFPEKDIQEKWFALLGF
SPEEAAEQFGFLLEAFETYGAPPHGGIALGLDRLWHLLAGRTNLRDTIAFPKTASASCL
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KASPESILTIALBESAAYFEKVKQYLINDLGISYEIDPINVRGADYYNHTYREIMSNAEG
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ARCFRDEDLRADRQPEFTQIDIEMSFMSQEDIMSLAEEMMAKVMRETKGEELQLPLPR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QNKINVKDAQTGEQIEVALDEFIHVMKANQKG"
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920. .6476
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                                                                                                                                                                                                                                                                                                                                                                                                       gene="hiss"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene="hiss"
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SASIVERAAKGDSYTITGSKGSWYEIKLDNGQTAYVAŇWVVQTSKSAEEAGEPPVSDS
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SEVVKRSSIPDRGVLEGDYYVLREINQPAMLYELGYVGHPQEEAIVHSNSYQEKVTOG
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                                                                                                                                                                                                                                                                                                                       Gapв
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                                                                                                                                                                                                                                                                                     Length 200707;
                                                                                                                                                                                                                                                                                      Score 457; DB 1; Length 20
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Best Local 8
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DEA"
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AGYVPLSALLPTLAPDNKGAAMSVLNLGSGLCAFIAPGIVSLFIGPLGAGGVIWIFAA
LYFFSAFLTRFLTISEQSTDVYTEERFVRENVQTNFDKTVKQ"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1783 TTGGCGCGGAAGTGGAGCACTATGAGCCGCTGCAGGTGCATGTGCAGCTTGAAAAGGTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1843 ATTTGGACGGCGATGTCACATTGAGCATAAGCATGAAAAAGTGTTTTCTATGGATGATT
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                                                                                                                                                                         gene
                                                                                                                                                                      note="sigma F/sigma G transcribed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=1
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/gene="orf4"
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Matches 613; Conservative
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Submitted (14-NOV-1995) S.M. Cutting, Dept. of Microbiology,
University of Pennsylvania School of Medicine, 346 Johnson
Pavillon, 3610 Hamilton Walk, Philadelphia, PA 19104-6076, USA
Location/Qualifiers
1. 2664
//organism="Bacillus subtilis"
//mol type="genomic DNA"
                       GTTTACGAAAATGCTGAATGTTACGGGGATCGGCCCCAAAAGGAGCGCTTGCGATCCTCGC
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                                                                                                                                                                                       22933 CTCGGGTGATCCCGGAGCGGTCATCCAAGCAATTGAAATGAAGATGAAGCTTTTTTGGT
                                                                                                                                                                                                                                            CAAATTTCCCGGCGTAGGCAAAAAAAGGGCAAGGCAGATCATCCTTGACCTGAAA 1055
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db_xref="UniProt/Swiss-Prot:005390"
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B.subtilis bofC, orfl, csbX, and orf4 genes.
X93081
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BofC encodes a putative forespore regulator subtilis sigma K checkpoint
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'db_xref="G1:1941917"
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Bacillus subtilis
Bacillus subtilis
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'db_xref="taxon:1423"
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transl_table=:
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/gene="csbX"
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Cutting, S.M.
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108746 CTACTTCGGAATTACGGACGATGGCACGTTGTCTTTTCAACGCAAACCGGGCCGGTC 108687
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                     darceccerricariteccerrearresecriceccerececeriadearearear 108927
                                                                    108926 TGTGCTCGAGCGGCAATACTTGGACGGAGATGAGCGAAGAGAAGTCACCGAAACCGT 108867
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GCTGGCCGCGCTCAGCTTTCACCTGGAGGCCTTGGCCGAAAAGCCGGGCTAAAGTTCAAAT 143
                                                                                                                                                                                              324 TTATATCGGAGTGACTGAAGATGGCGTGATTTCGACTTTTCACGGTCGCCCGGGCATCTT
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                                                                                                                     108866 CGATTCGATGACAGAAATATGGAAAAATATCGCGGTTGGCAACTCGTGACGCTCGATGA
                                                                                                                                                                                                                                                                                                                                             504 AGCCGTAAAATCATCCGGAAGCCAACATCATGTAGAAGATATGAAGACATGACGCTGTTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          858 TCGACAAGGGAAGAAAAATGCTGTTTACGAAAATGCTGAATGTTACGGGGATCGGCCCA
                                               CCAGCTTGAAAAGGTTTATCTGGACGGAGACGTTGGAATTGAGAATAAAGTAGAGGCCGC
                                                                                              204 TCGCACACTGGAAGACTTTAAAGCTGCTTGATAAAGGCTGGCAGCTCATCGATCAGAAAAA
                                                                                                                                              444 GGATGATCTGCGCAAAGGGATACCATACCGCACGAAAAAGGAATTTGAACATGTCATTGA
                                                                                                                                                                                                                                                                                                                                                                                            TGTCTTTTTCAGCTGCAGACAGAAGCTTTTTAGCGAACATATGTTAACTTTTTCATTC
                                                                                                                                                                                                                                                                                                                                                                                                                                            GAATTCGTAAAAGGGACGATTGATTAATGTATCGCCCCAATATATTGTCATTGAAAACGGC
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Best Local Similarity 54.0%; Pred. No. 4.6e-46;
Matches 528; Conservative 0; Mismatches 404;
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                              TGTCTTTTTCAGCTGCAGACAGAAGCTTTTTAGCGAACATATGTTAACCTTTTTCATTC
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Pred. No. 2.6e-42;
0; Mismatches 37; Indels 6;
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Methods for monitoring multiple gene expressi
Patent: WO 0229113-A 1616 11-APR-2002;
Novozymes Biotech, Inc. (US); Novozymes A/S
Location/Qualifiers

    .546
    .coganism="Bacillus licheniformis"
/mol_type="unassigned DNA"
/db_xref="taxon:1402"

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Pred. No. 4.6e-46;
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/ kdb_xref="G1:2987
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/db_xref="G1:29897928"
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MLIHITINSILFSIYKDPIALLFP"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement (2004. .3840)
/locus_tag="BC4290"
complement (2004. .3840)
/locus_tag="BC4290"
/EC_number="2.7.7.-"
/codon_start=1
/transI_table=11
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/locus_tag="BC4292"
complement (4202. .4333)
/locus_tag="BC4292"
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/codon_start=1
/transT_table=11
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Bacillus cereus ATCC 14579 section 15 of 18 of the complete genome.
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QTASKPEDIVKQSCTSCHGDQLQGAVGPNLQKIGGKLSKDEIKEILSKGKGNMPANIV
                                                                                                                                                                                                                          942 TCCGGCGATCCGGGAGCGGTGATTGAAGCGATCGAGAATGAGGACGAAGCATTTCT--CG 999
                                                                                                                     147 TTTACGAAATGCTGAATGTTACGGGGATCGGCCCAAAAGGAGCGCTGCCGATCCTCGCT 206
                                                                                                                                                                                                                                                                                                                          cereus group.

1 (bases 1 to 301332)

Ivanova, N., Sorokin,A., Anderson,I., Galleron,N., Candelon,B.,
Kapatral,V., Bhattacharyya,A., Reznik,G., Mikhailova,N.,
Lapidus,A., Chu,L., Mazur,M., Goltsman,E., Larsen,N., D'Souza,M.,
Walunas,T., Grechkin,Y., Pusch,G., Haselkorn,R., Fonstein,M.,
Bhilich,D.S.D., Overbeek,R. and Kyrpides,N.
Genome sequence of Bacillus cereus and comparative analysis with
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Kapatral,V., Bhattacharyya,A., Reznik,G., Mikhailova,N.,
Kapatral,V., Bhattacharyya,A., Reznik,G., Mikhailova,N.,
Bhattacharyya,A., Reznik,G., Mikhailova,N.,
Walunas,T., Grechkin,Y., Puen, Haelkorn,R., Fonstein,M.,
Ehrlich,D.S.D., Overbeek,R. and Kyrpides,N.
Submission
Submission
Submitted (12-MAR-2003) INRA, Genetique Microbienne, Domaine de
Vilvert, Jouy en Jossa 78352, France
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacillus cereus ATCC 14579
Bacillus cereus ATCC 14579
Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus, Bacillus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    267 CAATITINCCCGGCGTAGGCAAAAAACGGCAAGGCAGATCATCCTTGACCTGAAA 322
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Candelon, B., Gailloux, K., Ehrlich, D.S. and Sorokin, A.
The number of ribosomal RNA operons in Bacillus cereus
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/protein_id="AAP11201.1"
/db_xref="G1:29897927"
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/transT_table=11
/product="RNA polymerase sigma factor rpoD"
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| Corganism="Bacillus cereus ATCC 14579" |
| Mol_Lype="genomic DNA" |
| Ab_xref="ATCC 14579" |
| Ab_xref="ATCC:14579" |
| Ab_xref="Laxon:226900" |
| Complement | 114. 470 |
| Complement (114. 470 |
| Complement (114. 470 |
| Codon Start=1 |
| CransI_table=11
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complement(857, .196
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nasyglcncaertalfkavsegdkefvalavvadtkrpvppcgacrovmvelckodtk
vylsnlhgdvqettvgellpgaflaedlhe"
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Pred. No. 5e-34;
0; Mismatches 160; Indels 3;
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/locus_tag="BC4298"
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transl_table=
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Best Local Similarity 62.8%;
Matches 275; Conservative
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124149 TTTGAATATGTTACAGGTTACGTGGAGTATGTAGGGCCGGAATATGTCGTAATTGATCAT 124090
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Bacillus cereus ATCC 10987, section 15 of 18 of the complete
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Direct Submission
Submitted (19-FBB-2004) The Institute for Genomic Research, 9712
Medical Center Dr. Rockville, MD 20850, USA
Location/Qualifiers
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/nocus tag="bcE4553"
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                                                                                                                                           740
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ATCGAATTCGTAAAAGGGACGATTGATTATGTATCGCCCCAATATATTGTCATTGAAAAC
                                                                                                                                                                                                                                                                                      741 GGCGGGATCGGCTATCAGATCTTCACGCCAAATCCGTTTATTATAAGAAAAACAGCAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                  801 GAAA----CAATCTATACATACCATTATGTAAGAGAAGACACGAATGCGCTGTACGGCTTT
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NEGNICRERIKVEAVVNAAKEKGIPIRIGVNAGSLERHILLEKKGYPTADGMVESALHHI
KILEDLDFHDIJVSMKASDVNLAIEAYEKAARAFDYPLHLGITESCTLFAGTVKSAAG
SIGALISKGIGNTLRISLSADPVEEVKVARELLKSFGLASNAATLISCFTCGRIEIDLI
SIGALISKGIGNYLRALGLSADPVEEVKYARELLKSFGLASNAATLISCFTCGRIEIDLI
SIGALISKESTLOVPIKVAVLGCANNGFGEAREADIGIAGARGEGLLFRKGQVVRKV
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Complement (7502. .7915)

// locus tag="BCZ4359"
// locus tag="BCZ4359"
// note="identified by match to protein family HWM PF01475"
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ELFLLSFDEETAVSTGLSAKWIHFIFILLNAVSRRVGVLLVSSLMTLEVVASI
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LFKIVVPGSTFIYIAVVLIVLYLTIKEVPKPNEKNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="cation ABC transporter, permease protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="gcpE protein"
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/transT_table=:
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/transl_table=:
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GYTISRMEKWSGYTVIPFLSLLLFAIAVVLSFFVSKRECEGRYEVAQVLKERRIDKNW
GYTTRAHFFGGLREGFFIFVLSVYYLATDSELALGKYSLVNBAVSFVCYYLVARMLK
KENTRAHFFGGILYAVVEVJIFVYTKLLITAACIAIAYPILLVPYGSMTYDVIG
RAKNAREWRUSYVYNELWLANGRICSVLSFLCAVLFFPPEKSLPFLLIGAGHFLI
YFAVKNVKYDEGNAGNTSVVAQGTTQNQTEPEG"

COMPLEMENT (3816. .4427)
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/transl_table=11
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ATAIBAKFGSFPDAFREFAKAGATRFGSGHANLVVNNGELEVTSTPNQDSPLTEGKTF
VIGLDVWEHAYYLNYQNRRPDYIGAFWNVVDWNAAEKRYQEAK"
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/db_xref="d1:42739331"
/fb_xref="G1:42739331"
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/fb_xref="G1
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EIGRKANGERKETYNLTLVGYAPLEDPEVAFSVVVPWVDDKSGINGYISRDIMDAYFD
LKKVENGEATQEEIDKKNKKQDDE"
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TQNYVNLGLYNLASVVLQPLTPLIGGKLAKRIDRSILLRIGVGTLAIFFIVVLVAGKS
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/noTe="identified by match to protein family HMM PF00081;
match to protein family HMM PF02777"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             product="membrane protein, putative"
protein id="AAS43255.1"
/db_xref="G1:42739329"
                                                                                                                                            producE="penicillin-binding protein"
/protein_id="AAS41254.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement (2422, 3699)
/locus_tag="BCE4354"
complement (2422, 3699)
/locus_tag="BCE4354"
/codon_start=1
/transI_table=11
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complement(3816, .4427)
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product="tRNA-Met"
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4965. .5729
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/gene="tRNA-Met"
                                                                                                                 table=11
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transl_table=
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Pred. No. 9.7e-33;
0; Mismatches 163;
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Continuation <sup>(43</sup>
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Matches 272;
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/brotein_id="AAS43262.1"

/branslation="MNNILEIEGLSFRYEDRNVLEDINLQVPKGAFLGLVGPNGSGKS
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IVSKKGLFRFFTKNDKKKVBKALADVGMSEFGGRNIGELSGGQQQRVFIARALVSDPE
LILIDBEPVGGIDVKNVRSFYELLEDINKRLGTTLILVTHDMGAVTEKVTHVACLNQHL
HFHGNVEKFRELEDBEMSVLYGHHVHRLEHEHHHGRI"

complement (9713. .10591)
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                                                                                                                                       /locus tag="BCE4162"
note="identified by match to protein family HMM PF02588"
                                                                                                                                                                                                                                                                                                                                                           138033 TTTGAATATGTTACAGGTTACGTGGAGTATGTAGGACCGGAATATGTCGTAATTGATCAT
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                                                                                                                                                                                                                                                        3; Gaps
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                                                                                                                                                                                                                                DB 1; Length 288814;
                                                                                                                                                                                                                             Score 164.4; DB 1; Length
Pred. No. 1.4e-33;
0; Mismatches 161; Indels
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/protein_id="AAS43263.1"
                                                                                                               /locus_tag="BCE4362"
complement(9713. .10591)
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28466 TITGAATATGTTACGTGGAGTATGTAGGACGGAATATGTCGTAATTGATCAT 28407
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681 ATCGAATTCGTAAAAGGGACGATTGATTATGTATCGCCCCCAATATATTGTCATTGAAAAC 740
                                                                                                                                                                           GABARTCCGTGTCTATACATATCATTATGTGAGAGAAGATATTATGGCACTTTACGGGTTT
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15.3%; Score 161.2; DB 1; Length 110000;
Best Local Similarity 62.1%; Pred. No. 9.7e-33;
Matches 272; Conservative 0; Mismatches 163; Indels 3;
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Ger Copyright (c) nucleic search, usi February 27, 206 1 1 ccttaaggtaaggc e: 105510-408-1 1 ccttaaggtaaggc e: 105871174 NUC Gapop 10.0 , Gap 41078325 seqs, 2 41078325 seqs, 2 41078325 seqs, 2 41078325 seqs, 2 6 pleapth: 0 6 qlength: 0 6 qlength: 20000000 ing: Minimum Match 0 6 length: 20000000 ing: Minimum Match 1 Listing first 4 EST:* 1	.6 4.2 1101 10 CNS0039G AL063921 8 4.1 519 5 BQ496577 BQ496577 BQ496577 B .8 4.1 519 5 BQ501436 BQ501436 BQ501436 B .4 4.0 684 8 CX146914 CX146914 CX146914 I .4 4.0 738 8 CX153248 CX153248 CX153248 I .2 3.9 885 9 AZ574153 AZ574153 B .1 3.9 819 9 BH139275 BH139275 B .8 3.9 458 10 AG9315518 AG5915518 AG9315518 I .8 3.9 458 10 AG9315518 AG5915518 AG9315518 I .8 3.9 458 10 AG9315518 AG9315518 AG9315518 III AG9316518	3.9 468 10 AG938690 3.9 493 10 AG911866 3.9 546 10 AG944693 3.9 563 10 AG939340

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VERSION
KEYWORDS
SOURCE
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BH371812
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/dev stage="trifoliate"
/dev stage="trifoliate"
/dov stage="trifoliate"
/dorder lib="phosphate starved leaf"
/note="Vector: Lambda Zap; At the trifoliate stage, M.
truncatula plants were transplanted to phosphate-free sand
and grown for a further 30 days.
period, the plants were fertilized twice weekly with 1/2
Hoadlands solution containing only 20uM potassium
phosphate. RNA was prepared from above ground tissues."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Medicago truncatula (barrel medic)
Medicago truncatula
Spermatophyta; Magnoliophyta; eudicotyledona;
Spermatophyta; Magnoliophyta; Pabaceae; Papilionoideae; Trifolieae;
rosida; eurosida I; Pabalea; Pabaceae; Papilionoideae;
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                               506 AAGCGATCGTTTTCACCACTTTGTGGTGCGTGAAGACGCGCAGCTGCTGTACGGTTTTA 565
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              524 bp mRNA linear EST 19-MAR-20
NF047E06PLIF1049 Phosphate starved leaf Medicago truncatula CDNA
clone NF047E06PL 5', mRNA sequence.
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AAGAAACAATCTATACGATTATGTAAGAGAAGACACGAATGCGCTGTACGGCTTTT
                                                                             CGACAAGGGAAGAAAAATGCTGTTTACGAAAATGCTGAATGTTACGGGGATCGGCCCAA
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llarity 54.1%; Pred. No. 6.8e-08;
Conservative 0; Mismatches 118; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Harrison MJ
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402,
Tel: 580 221 7325
Fax: 580 221 7380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Medicago truncatula"
/mol_type="mRNA"
/db_xref="taxon:3860"
/clone="NP047E06PL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: mjharrison@noble.org
Insert Length: 524 Std Error: 0.00
Plate: 047 row: E column: 06
Seg primer: TCACACAGAAACAGCTATGAC.
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BG455392.1 GI:13378717
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799 AAGAAACAATCTATACCATTATGTAAGAGAAGACACGAATGCGCTGTACGGCTTTT 858

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Other GSSs: AG-ND-162110.TF

Contact: Brendan J Loftus

Contact: Brendan J Loftus

Contact: Brendan J Loftus

Contact: Brendan J Loftus

Department of Eukaryotic Genomics

Department of Eukaryotic Genomics

Department of Eukaryotic Genomic Research

Fax: 301 838 8238

Fax: 301 838 8243

Email: bjloftus@tigr.org

This clone is from an A. gambiae BAC library (ND-TAM) provided by FH. Collins and sequenced by The Institute for Genomic Research

F.H. Collins and sequenced by The Institute A: gambiae PEST strain

(TIGR). The BAC library was generated from A: gambiae PEST strain

(TIGR). The BAC library was generated from A: gambiae PEST strain

(TIGR). The BAC library was destracted from newly hatched first instar larvae

to minimize the inclusion of DNA from microorganisms that inhabit

the gut. The DNA is derived from mixed sexes of larvae. The BAC

library was constructed at Texas A&M Universty BAC Center

University, College Station, Texas 77843-2123, USA using a Hindili
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Bukaryota; Diptera; Nematocera; Culicoldea; Culicidae; Anophelinae; Anophelinae; Anophelinae; Anophelinae; Anophelinae; Anophelinae; Anophelinae; Anophelinae; Anophelinae; Anopheliae; Hong,Y.S., Hogan,J.K., Wang,X., Sarkar,A., Sim,C., Loftus,B.J., Ren,C., Huff,E.R., Carlile,J.L., Black,K., Zhang,H.-B., Gardner,M.J. and Collina,F.H. Construction of a BAC library and generation of BAC end sequence-tagged connectors for genome sequencing of the African malaria mosquito Anopheles gambiae

L. Mol. Genet. Genomics 268 (6), 720-728 (2003)
                                                                                                                                                                                                                                                                                                                                                                                979 AIGAGGACGAAGAITICICGICAAAITIICCCGGCGIAGGCAAAAAAGGGCAAGGGAGA 1038
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                                                                                                                                                                                                                                                                                                            318 Agrīgdcichtedcianichtercegaangreagcigeagcairíceiraandeceirdade 259
                                                                                                                                                                                                                                                                                                                                                                                                                              258 GIGAAGAAGIGGGGCACIGGIGAAACIGCCGGGTAITGGCAAAAAACGCCGGAACGCT 199
                                                                                                    859 CGACAAGGGAAGAAAAATGCTGTTTACGAAAATGCTGAATGTTACGGGGATCGGCCCCAA 918
378 acaaraacaadageecacarricricaaagagrigarcaaacgacgacgecgicge
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AG-ND-162110.TR ND-TAM Anopheles gambiae genomic clone
AG-ND-162110, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Anopheles gambiae (African malaria mosquito)
Anopheles gambiae
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/mol_type="genomic DNA"
/strain="PEST"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6.1%; Score 64;
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/clone="AG-ND-162110"
/clone_lib="ND-TAM"
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Seq primer: M13 Rev
Class: BAC ends.
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셤 ઠે qq ò g ò 셤 ò 셤

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286 AACATTTCATTGAAGATTGCAATAATTAAGAATGAGAATGATATTGAGAATGTATATGTG 227
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Best Local 8
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CX067472
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                                                                                                                                                                                                                                                                                   988 AAGCATTTCTCGTCAAATTTCCCGGCGTAGGCAAAAAAACGGCAAGGCAGATCATCCTTG 1047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CX137869 707 bp mRNA linear BST 03-JAN-2005
1277039 NCCCWA 03RT Oncorhynchus mykiss cDNA 5', mRNA sequence.
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Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified with
cross_match v0.990329.
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Rexroad, C. E., Rise, M., Koop, B., von Schalburg, K. and Yao, J. (3RT_rblb, NCCCWA/WVU EST Project, Phase II, in collaboration with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                           189 igitiakccaatrigregiececeaagarecceaacrecierarectricaaceataae 248
                                                        808 TCTATACATACCATTATGTAAGAAAGACACGAATGCGCTGTACGGCTTTTCGACAAGGG 867
                                                                                                                                                                    249 AAGAGCGCGCCGCTGTTTCGCGAGCTGATTAAAGTGAACGGCGTTGGCCCTAAACTGGCGC 308
                                                                                                                                                                                                                                            309 redecarrererecedarereacideageagrinareacidearreagearagaa 368
                                                                                                                                                                                                                                                                                                           369 TCACGTCGCTGATAAAATTGCCGGGGGTAGGAAAAACGCAGAGAGGCCTGGTGGTCG 428
                                                                                                                                                                                                         928 TTGCGATCCTCGCTTCCGGCGATCCGGGAGCGGTGATTGAAGCGATCGAGAATGAGGACG 987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    868 AAGAAAAATGCTGTTTACGAAAATGCTGAATGTTACGGGGATCGGCCCCAAAAGGAGCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Rexroad CE
USDA, ARS, National Center for Cool and Cold Water Aquaculture
11876 Leetown Road, KearneyBville, WV 25430, USA
Tel: 304 725 0351
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                     Indels
 Pred. No. 1.2e-06;
0; Mismatches 115;
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/organism="Oncorhynchus mykiss"
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Oncorhynchus mykiss
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Seq primer: ATTTAGGTGACACTATAG.
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/db_xref="taxon:8022"
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53.6%;
                     Matches 133; Conservative
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Best Local Similarity
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Best Local Similarity
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ACCESSION
VERSION
KEYWORDS
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ORGANISM
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491 AACATGTCATTGAAGCCGTAAAATCATCCGGAAGCCAACATCATGTAGAAGATATGAAGA 550

ORIGIN

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CAUB/472 468 bp mRNA linear EST 03-JAN-2005
1322268 NCCCWA 04RT Oncorhynchus mykiss cDNA, mRNA sequence.
CX067472
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii, Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
1 (bases 1 to 468)
Rexroad, C.E., Rise, M., Koop, B., von Schalburg, K. and Yao, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: crexroad@ncccwa.ars.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified with
cross match v0.990329.
Plate: 106 row: P column: 8
Seq primer: GTAATACGACTCACTATAGGG.
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//tab_nost_ruptv
//tone_lib='NCCURA 04RT"
/note="Vector: pCR 4-TOPO; This is an early neurogenesis
SSR library created by Mathew L. Rise constructed by
subtracting late neurogenesis (mixed stages: hindbrain
swelling + heart tube with peristalsis) from early
neurogenesis (mixed stages: neural groove + 1/2 epiboly).
Pish were from a domesticated strain (Spring Valley Trout
Parm, Langley, B.C.), courtesy of Bob Devlin, DFO. These
are mostly internal (coding) sequences."
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CATGACGCTGTTATGTCTTTTTTCAGCTGCAGACAGAAGCTTTTTTAGCGAACATATGTT 610
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                                                       226 CATTATGCAAGTTTTTTTTTTTTTATACAATGAAGATATTTTTGAGAGGAGTTATGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Rexroad CE
USDA, ARS, National Center for Cool and Cold Water Aquaculture
11876 Leetown Road, Kearneysville, WV 25430, USA
Tel: 304 725 0351
Pax: 304 725 0351
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                                                                                                                                                                                          AAAGATTTGCTTTTAATGCAGCATCAATTGTGATTTATAGAAAAGTACCCCAAG 113
                                                                                                                            611 AACTTTTCATTCTAGCTTTGCCTGTTTTGTGTTACAATGAAGAGCAGTCAAAG
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/mol_type="mRNA"
/db_xref="taxon:8022"
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Pred. No. 0.075;
0; Mismatches 7
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; asterids; lamiids; Solanales; Solanaceae; Solanum; Lycopersicon.

(bases 1 to 745)
Wang, C.K., Chen, P.Y., Wang, H.M., Soong, S.C., Chen, S.C. and To, K.Y.
DNA microarray profiling of gene expression during tomato root
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="Tomato CL5915 roots under different
                                                                                                                                                      Contact: Kin-Ying, To Contact: Kin-Ying, To Contact: Kin-Ying, To Crop Plant Improvement Group Crop Plant Improvement Group Institute of BioAgricultural Sciences, Academia Sin Institute of BioAgricultural Sciences, Academia Sin 188 Academia Rd. Section 2, Taipei, Taiwan 11529 Tel: 886-2-2653-3161 Fax: 886-2-2653-3161 Fax: 886-2-2653-3161 Fax: 886-2-2651-5600 Email: KytoAgate.sinica.edu.tw Insert Length: 75 Std Error: 0.00 Plate: 02 row: F column: 22 Seq primer: smart2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /dev stage="1-,2-,3-, and 4- month-old"
/lab_host="E.coli BM25.8"
                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Lycopersicon esculentum"
/mol_type="mRNA"
/cultivar="CL5915"
/db_xref="taxon:4081"
/clone="LE2TR02F22"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="roots"
                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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                                                                                                                                           Unpublished (2004)
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DEFINITION
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lycopersicon esculentum (Solanum lycopersicum)
Lycopersicon esculentum
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: crexroad@ncccwa.ars.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified with
cross match v0.990329.
Plate: 106 row: F column: 8
Seq primer: ATTTAGGTGACACTATAG.
                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus. 1 (Bases I to 485) ** Rexroad, C.E., Rise, M., Koop, B., von Schalburg, K. and Yao, J. (ART grool, NCCCWA/WVU EST Project, Phase II, in collaboration with
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/lab_host="Topia"
/clone_lib="WCCCWA 04RT"
/clone_lib="WCCCWA 04RT"
/note="Vector: pCR 4-TOPO; This is an early neurogenesis
subtracting late neurogenesis (mixed stages: hindbrain
swelling + heart tube with peristalsis) from early
neurogenesis (mixed stages: neural groove + 1/2 epiboly).
Fish were from a domesticated strain (Spring Valley Trout
Farm, Langley, B.C.), courtesy of Bob Devlin, DFO. These
are mostly internal (coding) sequences."
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                                                                                                                                                                                                                                                                                                                                                                                          Contact: Rexroad CE
USDA, ARS, National Center for Cool and Cold Water Aquaculture
11876 Leetown Road, Kerneysville, WV 25430, USA
Tel: 304 724 8340 x2129
Fax: 304 725 0351
                                                                   СХ067473
1322269 NCCCWA 04RT Oncorhynchus mykiss cDNA, mRNA sequence.
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                                                                                                                                                                             Oncorhynchus mykiss (rainbow trout)
Oncorhynchus mykiss
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/db_xref="taxon:8022"
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                                                                                                                                           CX067473.1 GI:56989039
                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (2004)
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1101 bp DNA linear GSS 03-JUN-1999
Drosophila melanogaster genome survey sequence TET3 end of BAC #
BACROSKIO of RPCI-98 library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
developmental stages"

//note="Vector: pTriplEx2; Tomato CL5915 seeds are obtained fnote="Vector: pTriplEx2; Tomato CL5915 seeds are obtained from aVRDC. Rocts were harvested from plants grown under different developmental stages: 1-,2-,3-,4-month-old.

Equal aliquots of mRNA of different developmental stages were mixed and used for cDNA library construction. (Smart pCR cDNA Library construction. (Smart pCR cDNA Library construction.
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                                                                                                                                                                                                                                                                     DB 7; Length 745;
                                                                                                                                                                                                                                                                     4.3%; Score 45.8; DB 7; Length 7<sup>,</sup> Local Similarity 47.6%; Pred. No. 0.19; ndels nes 169; Conservative 0; Mismatches 182; Indels
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BQ496577.1 GI:24447391
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Matches 83; Conservative
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Li Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr

Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Gosegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo.

NY. The library is named RPCI-98 and was constructed by partial Econer Genetics at the Roswell Park Cancer Institute in Buffalo.

NY. The Library is named RPCI-98 and was constructed by partial BCORI digestion of Drosophila DNA provided by the BDGP from the isogenic strain v2; cn bw sp, the same strain used for the BDGP's pland BCT library and how to order individual BAC clones, the entire library, and how to order individual BAC clones, the entire library, and how to order individual EACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  818 RDWGDRAGKRGGARKRRDRKRADDKRDAADDRDDAATWTTTTTTRDTDDWKWKTDTWT
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                                     Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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/organism="Drosophila melanogaster"
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1 Similarity 14.5%; Pred. No. 0.46;
62; Conservative 194; Mismatches 171;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACR08K10"
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/note="end : TET3"
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8Q496577 501 bp mRNA linear EST 31-OCT-2002 EST05806 Pb0001 Paracoccidioides brasiliensis cDNA, mRNA sequence.
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Expressed sequence tag analysis of the human pathogen
Paracoccidioides brasiliensis yeast phase: identification of
putative homologues of Candida albicans virulence and pathogenicity
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                                                                                                                                                                                                            Bukaryota; Fungi; Ascomycota; Pezizomycotina; Burotiomycetes; Onygenales; mitosporic Onygenales; Paracoccidioides.

[ Dases 1 to 501)
Goldman,G.H., dos Reis Marques,E., Duarte Ribeiro,D.C., de Sou Bernardes,L.A., Quiapin,A.C., Vitorelli,P.M., Savoldi,M., Semighini,C.P., de Oliveira,R.C., Nunes,L.R., Travassos,L.R., Puccia,R., Batista, M.L., Ferreira,L.B., Moreira,J.C., Bogesian,A.P., Tekaia,F., Nobrega,M.P., Nobrega,R.G. and
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Paracoccidioides brasiliensis

Bukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;

Onygenales; mitosporic Onygenales; Paracoccidioides.

1 (baees 1 to 519)

Goldman, G.H., dos Reis Marques, E., Duarte Ribeiro, D.C., de Sou Bernardes, L.A., Quiapin, A.C., Vitorelli, P.M., Savoldi, M., Semighini, C.P., de Oliveira, R.C., Nunes, L.R., Travassos, L.R., Puccia, R. Batista, W.L., Ferreira, L.B., Moreira, J.C.,

Bogossian, A.P., Tekaia, F., Nobrega, M.P., Nobrega, F.G. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Gustavo Henrique Goldman
Laboratory of Molecular Biology
Universidade de Sao Paulo - USP - PCFRP
VA Ó Cafe S/N, CEP: 14040-903, Ribeirao Preto - SP, Brazil
Email: ggoldman@usp.br
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EST10661 Pb0001 Paracoccidioides brasiliensis cDNA,
BQ501436

    .501
    /organism="Paracoccidioides brasiliensis"

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/db_xref="taxon:121759"
/clone_lib="Pb0001"
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                                                                                                                                                   Paracoccidioides brasiliensis
Paracoccidioides brasiliensis
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1. .527
/organism="Homo sapiens"
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CX146914/c
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Fax: 319 356 471
Email: paul-mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa CDNA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com) or from Open Biosystems
(www.openbiosystems.com)
Seq primer: MI3 FORWARD
POLYA=NO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CB853944 527 bp mRNA linear EST 22-APR-2003
UI-CF-DU1-aak-p-13-0-UI.81 UI-CF-DU1 Homo sapiens cDNA clone
                         Expressed sequence tag analysis of the human pathogen paracoccidioides brasiliensis yeast phase: identification of putative homologues of Candida albicans virulence and pathogenicity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    754 ATCAGATCTTCACGCCAAATCCGTTTATTATAAGAAAAACAGCAAAGAAACAATCTATA 813
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini;
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1 (bases 1 to 527)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
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Laboratory of Molecular Biology
Universidade de Sao Paulo - USP - FCFRP
Av do Cafe S/N, CEP: 14040-903, Ribeirao Preto - SP, Brazil
Email: ggoldman@ugp.br.
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Pred. No. 1.2;
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4.1%; Score 42.8; Di
Best Local Similarity 55.3%; Pred. No. 1.2;
Matches 83; Conservative 0; Mismatches
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                                                                                              Eukaryot. Cell 2 (1), 34-48 (2003)
12582121
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Contact: McCray, PB
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                  Goldman, M.H.
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/dev stage="Adult"
/lab_host="DHIOB (Life Technologies) (T1 phage resistant)"
/lab_host="DHIOB (Life Technologies) (T1 phage resistant)"
/lab_host="DHIOB (Life Technologies) (T1 phage resistant)"
/clone lb="Ur-Gr-DHIO"
/note="Organ: Lung: Vector: pT7T3-Pac (Pharmacia) with a
/note="Organ: Lung: Vector: pT7T3-Pac (Pharmacia) with a
/note="Organ: Lung: Site_1: EcoR I; Site_2: Not I;
modified polylinker; Site_1: EcoR I; Site_2: Not I;
modified polylinker; Site_1: EcoR I; Site_2: Not I;
modified polylinker; Site_1: EcoR I; Site_2: Not I;
modified conneme Research, 6:79:1-806. 1996. First strand
Soares (Genome Research, 6:79:1-806. 1996. First strand
containing a Not I site. Double stranded cDNA was ligated
to an EcoR I adaptor, digested with Not I, and cloned
directionally into pT7T3-Pac vector. The oligonucleotide
used to prime the synthesis of first-strand cDNA contains
a library tag sequence that is located between the Not I
site and the (dT)!B tail. The sequence tag for this
TAG_SEQ=None found"
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Fax: 304 725 0351
Email: crexroad@ncccwa.ars.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option., Vector identified with
cross_match v0.990329.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               945 GGCGATCCGGGAGCGGTGATTGAAGCGATCGAGAATGAGGACGAAGCATTTCTCGTCAAA 1004
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CX146914
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USDA, ARS, National Center for Cool and Cold Water Aquaculture
11876 Leetown Road, Kearneysville, WV 25430, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTAAGAGAAGACACGAATGCGCTGTACGGCTTTTCGACAAGGAAGAAAAAATGCTGTTT
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/mol_type="mRNA"
/db_xrefe"taxon:9606"
/clone="UI-CF-DUI-aak-p-13-0-UI"
/tissue_type="Primary Lung Epithelial Cells"
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4.1%; Score 42.8; DB 6;
Best Local Similarity 49.1%; Pred. No. 1.2;
Matches 113; Conservative 0; Mismatches 117;
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Oncorhynchus mykiss
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Gaps

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Length 701;

355

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Eukaryotan, Merazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Actinopterygii, Neopterygii, Teleostei, Euteleostei, Portacanthopterygii, Salmoniformes, Salmonidae, Oncorhynchus.

1 (bases 1 to 738)

Rexroad, C. E., Rise, M., Koop, B., von Schalburg, K. and Yao, J.

OSRT_rblb, NCCCWA/WVU EST Project, Phase II, in collaboration with
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/note="Vector: pBluescript SK+; This is a normalized (Cot = 5) 0. mykiss whole juvenile library created by Matthew L. Raise from approximately 4 month old 0. mykiss (Tzenzaicut Lake strain) obtained from Vancouver Island Trout Hatchery (Duncan, B.C.)."
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   /clone_lib="NCCCWA 03RT"
/note="Vector: pBluescript SK+; This is a normalized (Cotes"Vector: pBluescript SK+; This is a normalized (Cotes) of mykiss whole juvenile library created by Matthew L. Rise from approximately 4 month old O. mykiss (Tzenzaicut Lake strain) obtained from Vancouver Island Trout Hatchery (Duncan, B.C.)."
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1293858 NCCCWA 03RT Oncorhynchus mykiss CDNA 3', mRNA sequence.
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Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified
cross_match v0.90329.
Plate: 131 row: B column: 19
Seq primer: GTAATACGACTCACTATAGGG.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 177 TGGAATTGAGAATAAAGTAGAGGCCGCTCGCACACTGGAAGACTTTAAAGCTGCTTATAA
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USDA, ARS, National Center for Cool and Cold Water Aquaculture
11876 Leetown Road, Kearneysville, WV 25430, USA
Tel: 304 725 0351
Fax: 304 725 0351
                                                                                                                                                                                                                                                                                                         Query Match 4.0%; Score 42.4; DB 8; Length 7 Best Local Similarity 49.5%; Pred. No. 1.7; Matches 109; Conservative 0; Mismatches 111; Indels
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/organism="Oncorhynchus mykiss"
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Oncorhynchus mykiss
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/db_xref="taxon:8022"
/tissue_type="pooled"
/lab_host="DH108"
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CX153248.1 GI:57009903
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Plate: 117 row: G column: 22
Seq primer: GTAATACGACTATAGGG.
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Oncorhynchus mykiss
Bukaryota, Metazoa, Chordata, Craniata; Vertebrata; Buteleostomi;
Actinopterygii, Neopterygii; Teleostei; Buteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
I (bases I to 701)
Rexroad, C. B., Rise, M., Koop, B., von Schalburg, K. and Yao, J.
ONRT rblb, NCCCWA/WVU EST Project, Phase II, in collaboration with
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Contact: Rayload CE
Contact: Rayload Center for Cool and Cold Water Aquaculture
11876 Leetown Road, Kearneysville, WV 25430, USA
Tel: 304 724 8340 x2129
Fax: 304 725 0351
Email: crexroad@ncccwa.ars.usda.gov
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1284312 NCCCWA 03RT Oncorhynchus mykiss CDNA 3', mRNA sequence.
CX144590
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    /organism="Oncorhynchus mykiss"

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Plate: 120 row: M column: 2
Seg primer: GTAATACGACTCACTATAGGG.
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/db_xref="taxon:8022"
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/db_xref="http://db.
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/dlone lib="Entamoeba histolytica Sheared DNA"
/dlone lib="better by Site_1: Bst 1; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond (Clark,
C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a
method for isolate identification. Exp. Parasitol.
77:450.). The DNA was mechanically sheared to give a
tight size distribution (-2 kb). The v + i method used for
the library construction is described in detail in Smith,
H.O. and Venter, J.C. (Making small insert libraries for
whole genome shotgun sequencing projects. In Genome
Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barell, Oxford University Press, 1999)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Entamoeba histolytica
Entamoeba histolytica
Entamoeba histolytica
Entamoeba histolytica
Eukaryota; Entamoebidae; Entamoeba.
E (bases 1 to 882)
Loftus, B., Van Aken, S. and Fraser, C.
Determination of clone end sequences from Entamoeba histolytica
HM1:IMSS sheared DNA library
Unpublished (2000)
Lonbarct: Brendan J Loftus
Contact: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 9543
Email: bjoftus@tigr.org
Clones are derived from the Entamoeba histolytica HM1:IMSS sheared
DNA library
Seq primer: M13-Reverse
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B82 bp DNA linear GSS 14-DEC-2000 ENTWUG4TR Entamoeba histolytica genomic, genomic survey sequence.

AZ674153.1 GI:11811299
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High quality sequence start: 17
High quality sequence stop: 647.
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/strain="HM1:IMSS"
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nes 109; Conservative
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3.9%; Score 41.2; DB 9; Length 882; 51.6%; Pred. No. 4;

Query Match Best Local Similarity

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  0; Mismatches
  94; Conservative
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  Matches
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February 27, 2006, 06:31:46; Search time 745 Seconds (without alignments) 9437.920 Million cell updates/sec
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GenCore version
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Adn60329 B. lichen	Adg32153 DNA encod	Abk75799 Bacillus	Abk74325 Bacillus	Abk78681 Bacillus	Continuation (16 o	Continuation (16 o	Continuation (2 of	Continuation (15 o	Continuation (6 of	Adb11501 Alloiococ	Adb11499 Alloiococ	Abn91317 Staphyloc	Ads01069 Staphyloc	Abz42153 Streptoco	Aav52173 Streptoco	Abs56454 Streptoco	Abx05796 S. pneumo	Acf72471 Staphyloc
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Score	1055	1055	459	195.4	137	124.8	122	122	108.2	107.6	104.8	104.8	103.4	103.4	89.8	89.8	89.8	89	83
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The invention relates to a Bacillus licheniformis mutant host cell derived from a parent B. licheniformis host cell. The mutant host cell is mutated in one or more genes encoding one or more polypeptides involved in sporulation. The host cell comprises one or more heterologous genes in sporulation. The host cell comprises one or more heterologous genes present in at least two copies, encoding one or more heterologous polypeptides. The heterologous genes are stably integrated into the genome of the cell without leaving any antibiotic resistance marker genes

Disclosure; SEQ ID NO 1; 319pp; English.

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at the site of integration. The heterologous genes are transcribed from a heterologous promoter or from an artificial promoter, and are comprised in an operon, preferably a polycistronic operon. The heterologous polypeptide is an antimicrobial peptide, or a fusion peptide comprising a poptide part which in its native form has antimicrobial activity. The heterologous polypeptide is an enzyme, preferably a secreted enzyme. The heterologous polypeptide is an enzyme, preferably a secreted enzyme. The enzyme of a class selected from the group of enzyme classes consisting of oxidoreductases (BC 1), transferases (BC 2), hydrolases (BC 3), lyasses (EC 4), isomerases (BC 5), and ligases (BC 6). The Bacillus licheniformis is useful in a process for producting at least one product of interest, comprising cultivating a B. licheniformis mutant host cell in a suitable medium, whereby the said product is produced. The process further comprises isolating or purifying the product of interest. The current sequence represents a B. licheniformis sporulation related polynucleotide

Sequence 1055 BP; 325 A; 208 C; 259 G; 263 T; 0 U; 0 Other;

Gape DB 12; Length 1055; ö 0; Indels Query Match 100.0%; Score 1055; DB 12; Best Local Similarity 100.0%; Pred. No. 9.8e-314; Matches 1055; Conservative 0; Mismatches 0;

9 CCTTAAGGTAAGGCAAAAAAGAAGGTGATATTGATGTACAGCCGAAGCAAGTTCAAAATC

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AAGCGGCTGGAAAGCCGGATGGTGATCTGCGCAAAGGGATACCATACCGCACGAAA

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AATATATTGTCATTGAAAACGGCGGGATCGGCTATCAGATCTTCACGCCAAATCCGTTTA AATATATTGTCATTGAAAACGGCGGATCGGCTATCAGATCTTCACGCCAAATCCGTTTA

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AACATATGTTAACTTTTTCATTCTAGCTTTGCCTGTTTTGTGTTACAATGAAGAGCAGTC AACATATGTTAACTTTTTCATTCTAGCTTTGCCTGTTTTGTGTTACAATGAAGAGAGTC 601 601 661

BP. ADG32153 standard; DNA; 1522 (first entry) 26-FEB-2004 ADG32153; RESULT 2 ADG32153

DNA encoding a mutant B_licheniformis secreted polypeptide SeqID 123. mutant; host cell; production yield; shelf life; product stability; purity; secreted; gene; ds.

Synthetic. Bacillus licheniformis.

WO2003093453-A2.

13-NOV-2003

25-MAR-2003; 2003WO-DK000198

360

360

10-APR-2002; 2002DK-00000534

(NOVO) NOVOZYMES AS

Andersen JT, Jorgensen ST,

ŏ New mutant Bacillus licheniformis host cell secreting 5 % less of more secreted polypeptides than the parent host cell, useful for producing a product of interest e.g. polypeptides, amino acids or carbohydrates. 2004-053045/05. P-PSDB; ADG32154

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Clausen IG;

Olsen PB,

Rasmussen MD,

Disclosure; SEQ ID NO 123; 422pp; English.

This invention relates to a novel Bacillus licheniformis (B. licheniformis) mutant host cell derived from a parent B. licheniformis host cell that is mutated in genes encoding secreted polypeptides. Specifically, it refers to the generation of an improved Bacillus host that reduces the need for product purification caused by contaminant secreted native polypeptides in the culture medium. Accordingly, the present invention describes reducing the expression of these mative proteins (e.g. proteolytic enzymes, nutrient uptake factors and signal molecules), which in turn makes it easier to purify the heterologous product of interest and therefore improving the production process. Further benefits of a mutated host cell include an increase in total production yield and a longevity of shelf life attributable to improved product stability and purity. This polynucleotide is a DNA sequence

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Best Local Similarity
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ive 0; Mismatches 0;
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The invention describes a method of monitoring differential expression of the genes in a first Bacillus cell relative to expression of the genes in cother Bacillus cells to a substrate containing array of Bacillus isolated from Bacillus cells to a substrate containing array of Bacillus cales isolated from Bacillus cells to a substrate containing array of Bacillus cells to a substrate some determining to a spot in the array. The method is useful for measuring the expression of a spot in the array. The method is useful for monitoring contains or more second Bacillus cells. The method is useful for monitoring global expression of several genes from a Bacillus cell, discovering new genes, identifying possible functions of unknown open reading frames and contituding ene copy number variation and stability. Monitoring changes in expression of genes may be used to provide a representation of the way in which Bacillus cells adapt to changes in culture conditions, contituonmental stress or other physiological provocation. Extensive follow continumental stress or other physiological provocation. Extensive follow continumental stress or other physiological provocation. Extensive follow continumental stress or other physiological provocation is available.

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This sequence represents a genomic sequence information is available.

This sequence represents a genomic sequence information is available.

The invention. Note: The sequence data for this patent did not form to part of the printed specification, but was obtained in electronic format continuence.
Monitoring differential expression of several genes in first Bacillus cell relative to expression of same genes in one or more second Bacillus cells, by using substrate containing Bacillus genomic sequenced tag
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27-MAR-2001; 2001US-0279526P.
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61 AGCCGGCTAAAGTTCAAATCCAGCTTGAAAAGGTTTATCTGGACGAGACGTTGGAATTG 120
                                                                                                                                                                             AGAATAAAGTAGAGGCCGCTCGCACACTGGAAGTTTAAAGCTGCTTATAAAGGGTGGC 180
                                                                                                                                                                                                                                                                                                                                                                 301 ACGGTCGCCCGGGCATCTTATCAGAACCCATTCAATCGTTTTTTCAGATTGATATAAAGC 360
                                                                                                                                                                                                                                                                                                                                                                                                                 GGCTGGAAAAGCCGGATGGGGATGATCTGCGCAAAAGGGATACCATACCGCACGAAAAAAGG 420
                             65 TATTGCTTATTGGAAGTCTGCTGGCCGCGCTCAGCTTTCACCTGGAGGCCTTGGCCGAAA 124
                                                                                                                                                     AGAATAAAGTAGAGGCCGCTCGCACACTGGAAGACTTTAAAAGCTGCTTATAAAGGGTGGC 244
                                                                                                                                                                                                               AGCTCATCGATCAGAAAAAGGGGTTTATTCTGTTTCGCAAACAGGTGGACGACATTTCTC 304
                                                                                                                                                                                                                                             AGCTCATCGATCAGAAAAAGGGGTTTATTCTGTTTCGCAAACAGGTGGACGACATTTCTC 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       coring differential expression of several genes in first Bacillus relative to expression of same genes in one or more second Bacillus s, by using substrate containing Bacillus genomic sequenced tag
                                                          1 TATTGCTTATTGGAAGTCTGCTGGCGCGCTCAGCTTTCACCTGGAGGCCTTGGCCGAAA
                                                                                         125 AGCCGGCTAAAGTTCAAATCCAGCTTGAAAAGGTTTATCTGGACGGAGACGTTGGAATTG
                                                                                                                                                                                                                                                                                                                                       ACGGTCGCCCGGGCATCTTATCAGAACCCATTCAATCGTTTTTTCAGATTGATATAAAGC
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0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           AATTTGAACATGTCATTGAAGCCGTAAAATCATCCGGAA 523
0; Mismatches
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27-MAR-2001; 2001US-0279526P.
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459; Conservative
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The invention describes a method of monitoring differential expression of genes in a first Bacillus cell relative to expression of the genes in cother Bacillus cells, comprising hybridising labelled nucleic acid probes isolated from Bacillus cells to a substrate containing array of Bacillus genomic sequenced tags (GST), examining the array, and determining a spot in the array. The method is useful for measuring the expression of a spot in the array. The method is useful for monitoring can one more second Bacillus cells. The method is useful for monitoring genes in a first Bacillus cells. The method is useful for monitoring calobal expression of several genes from a Bacillus cell, discovering new genes, identifying possible functions of unknown open reading frames and monitoring gene copy number variation and stability. Monitoring chemes in which Bacillus cells adapt to changes in culture conditions, in which Bacillus cells adapt to changes in culture conditions.

This sequence represents a genomic sequence information is available. This sequence represents a genomic sequence tag (GST) used in the method of the printed specification, but was obtained in electronic format partectly from WIPO at ftp. wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CGCCAAATCCGTTTATTATAAGAAAAACAGCAAAGAAACAATCTATACATA---CCATT
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                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 546 BP; 165 A; 123 C; 141 G; 116 T; 0 U; 1 Other;
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06-OCT-2000; 2000US-00680598

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(NOVO ) NOVOZYMES AG.

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(NOVO ) NOVOZYMES AG.

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WPI; 2002-416684/44.

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WPI; 2002-416684/44.

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WPI; 2002-416684/44.

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WPI; 2002-416684/44.

XX
Monitoring differential expression of several genes in first Bacillus cells by using substrate containing Bacillus genomic sequenced tag array.

Claim 11; SEQ ID NO 5972; 200pp; English.

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Claim 11; SEQ ID NO 5972; 200pp; English.

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Claim 11; SEQ ID NO 5972; 200pp; English.

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Claim 12; SEQ ID NO 5972; 200pp; English.

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Claim 13; SEQ ID NO 5972; 200pp; English.

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Claim 14; SEQ ID NO 5972; 200pp; English.

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Claim 15; SEQ ID NO 5972; 200pp; English.

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Claim 16; SEQ ID NO 5972; 200pp; English.

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Claim 17; SEQ ID NO 5972; 200pp; English.

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Claim 18; SEQ ID NO 5972; 200pp; English.

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Claim 19; SEQ ID NO 5972; 200pp; English.

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Claim 10; SEQ ID NO 5972; 200pp; English.

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679 TGATCGAATTCGTAAAAGGGACGATTGATTATGTATCGCCCCCAATATATTGTCATTGAAA
                                                                                                                                             4 TGATTGATTATATAAAGGGAATTTGGTTGCAGTTGAACCTGCTTATCTCGTGGTCGAGA
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ABQ69245 15/c ContinuaTion (16 of 31) of ABQ69245 from base 1500001 (Listeria innocua DNA sequence #68 WP Sequence split into 31 fragments LOCUS ABQ69245 Accession Abg69245

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Oy Db 6	708	ATGTATCG	tatgtatggccccaatatattgtcattgaaaacggcggatggctatcaggtctcacg 	ATTG	rcarrga rrgrrga	AAACG GGCAG	GCGGG H GACAA	ATCGGC ATCGGC	TATC	AGATC AAATA	TTCACG ATTACA	767	36	
oy da	768	CAAATCCG GGAACCCG	ccaaatccgtttattataagaaaaacagcaaagaaacaatctatacatacat 	PAAGA-	A sactaga	AAACA AGGTA	GCAAA CAGAA	-aaaacagcaaagaaacaatctatacata 	ATCT.	ATACA TTTTG	TACCAT TATCAG	821	92	
oy Ob	822	TATGTAAGA CATGTGAGA	tatgtaagagagacacgaatgcgctgtacggcttttcgacaagggaagaaaaatgctg 	AATGC	GCTGTA	7667 	TTTCG	ACAAGG ACAACA	GAAG 	AAAAA 	ATGCTC TATTI	3 881 A 6881	91	
oy Oy	882 8815	TTTACGAAA TTCAAAAAA	tttacgaaaatgctgaatgttacggggatcggcccaaaaggagggcttgggatcctcg 	GTTAC	GGGGAT GGGCAT	CGGCC TGGAC	CAAAA	GGAGCG AGCGCA	SCTTG 	CGATC CCATT	CTCGCT ATTGCT	941	99	
o o o	942 T 8755 T		ccgccartccggagcggtgattgaagcgatcgagaatgagagcgaagcatttctcg 	GTGA1	TGAAGC	GATCG	AGAAT AATCC	GAGGAC GAAGAC	CAAG 	CATTT TTTAT	CGT	100	1 96	
e Sp	1002 A 68695 A	AATTTCCC AATTTCCG	aartticccgcctaggcaaaaaacggcaaggcagatcatccttgacctgaa 	AAAA	VAACGGC	AAGGC TCGCC	AGATC	cggcaaggcagatcatccttgacctgaaa 	GACC	TAAAA	1055	Ο.		

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RESULT 9
ADB12064 14/C
Continued in (15 of 18) of ADB12064 from base 1400001 (Alloiococcus otitis entire genome WP Sequence split into 18 fragments LOCUS ADB12064 Accession Adb12064
WP Fragment Name Begin 110000
WP ADB12064 00 1 100000
WP ADB12064 01 200001 310000
WP ADB12064 03 300001 310000
WP ADB12064 04 400001 310000
WP ADB12064 05 500001 510000
WP ADB12064 07 700001 810000
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                                                                                    Length 110000;
                                                                                    Score 122; DB 6; Length 11
Pred. No. 2.7e-25;
0; Mismatches 150; Indels
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Pred. No. 4.8e-21;
0; Mismatches 183;
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Matches 247; Conservative
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                                                                                Query Match
Best Local Similarity
Matches 228; Conser
ABQ67195_2
ABQ67195_3
ABQ67195_4
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Pred. No. 2.7e-25;
0; Mismatches 150; Indels
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Continuation (2 of 5) of ABQ67195 fire
WP Sequence split into 5 fragments
WP Fragment Name Begin
WP ABQ67195_0
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WP ABQ67195_1
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nes 228; Conservative
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ABQ69245 01
ABQ69245 02
ABQ69245 03
ABQ69245 04
ABQ69245 05
ABQ69245 05
ABQ69245 06
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ABG69245_15
ABG69245_16
ABG69245_17
ABG69245_19
ABG69245_19
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ABQ69245_24
ABQ69245_25
ABQ69245_26
ABQ69245_27
ABQ69245_27
ABQ69245_29
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ABQ69245_10
ABQ69245_11
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ABQ69245_21
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The present invention describes an isolated polymucleotide (I) of Allolococcus otitidis genomic DNA, which encodes an antigenic protein. Allolococcus otitidis ganomic DNA, which encodes an antigenic protein. Allolococcus otitidis is a gram-positive bacterium. Also described: (1) an isolated polypeptide that is encoded by the polymucleotide (I), its complement, despenarate variant or fragment; (3) a genetically engineered composition comprising the polypeptide of (1); (5) an immunogenic composition comprising the polypeptide of (1); (5) an immunogenic composition comprising the polypeptide, its composition comprising the polypeptide of (1); (6) a pharmaceutical composition comprising the captression vector; (6) a pharmaceutical composition comprising the copyreptide of (1); their biological equivalent or fragment; (8) communishing against Allolococcus otitidis by administering to a host the immunogenic composition; (9) detecting and/or identifying Allolococcus otitidis in the biological sample; (10) a kit comprising a container. Containing the novel polymucleotide, its degenerate variant or fragment, or the antibody of (4); and (11) producing a polypeptide by culturing the containing the novel polymucleotide, its degenerate variant or fragment. Co the antibody of (4); and (11) producing a polypeptide by culturing the polymucleotides, onlypeptide and compositions of the present polymucleotides, antibodies and diagnosing diagnesses, drug screening assays and monitoring of effects during detecting Alloicoccus otitidis antigen contidis. The present sequence encodes an Alloicoccus otitidis antigen
                                                                                            TGGCTAGTGCAATTCAAAATGGTGAAGTAAAATACCTGACTCGTTTCCCGGGAGTAGGAA 12007
    11888 TTTCAGGAATTGGACCTAAGTCTGCTGGCAATTATGGCTGCTGAAGATACTGATTCTT 11947
                                                 TGATTGAAGCGATCGAGAATGAGGACGAAGCATTTCTCGTCAAATTTCCCGGCGTAGGCA 1020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New Alloiococcus otitidis polynucleotides and polypeptides, useful for treating and diagnosing diseases, drug screening assays and monitoring effects during drug clinical trials.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alloiococcus otitidis, antigenic protein; immunogenic; immunisation; gene therapy, Gram-positive bacterium; infection; gene; ds.
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18-NOV-2002; 2002US-0426742P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New Alloiococcus otitidis polynucleotides and polypeptides, useful for
                                                                               TTTATCTGTGTATAATAAAATGACTATTGGAAAAAGTGGTGAAAGTA---TGTATGAAT
                                                                                                                       688 TCGTAAAAGGGACGATTGATTATGTATCGCCCCAATATATTGTCATTGAAAACGGCGGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alloiococcus otitis antigenic protein encoding DNA SEQ ID NO:5563
                                                           9;
                                      Length 654;
                   Sequence 654 BP; 192 A; 148 C; 155 G; 159 T; 0 U; 0 Other;
                                     Score 104.8; DB 9; Length
Pred. No. 3.3e-21;
0; Mismatches 182; Indels
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protein from the present invention.
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                                     Best Local Similarity 56.0%;
Matches 243; Conservative (
                                                                                                                                                                                                                                                                                                                                                                           TCCTTGACCTGAAA 1055
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The present invention describes an isolated polynuciecture.
Alloiococcus otitidis genomic DNA, which encodes an antigenic protein.
Alloiococcus otitidis is a Gram-positive bacterium. Also described: (1)
Alloiococcus otitidis is a Gram-positive bacterium. Also described: (1)
Can isolated polypeptide that is encoded by the polynuciectide (1); (2) an expression vector comprising the novel isolated polynuciectide (1); its complement, degenerate variant or fragment; (3) a genetically engineered composition comprising the polypeptide of (1); (5) an immunogenic composition comprising the polypeptide of (1); (5) an immunogenic composition comprising the polypeptide of (1) and a carrier; (7) a protein char is comprising the expression vector; (6) a pharmaceutical composition comprising the carrier; (7) a protein char is comprising the polypeptide of (1), their biological equivalent or fragment; (8) immunogenic composition; (9) detecting and/or identifying Alloiococcus otitidis in the biological sample; (10) a kit comprising a container containing the novel polymeticotide, its degenerate variant or fragment, or the antibody of (4); and (11) producing a polypeptide by culturing the polymucleotides, polypeptides, antibodies and compositions of the present invention can be used for treating and diagnosing diseases, drug creening assays and monitoring of effects during drug clinical trials.

The polymucleotides are useful for expressing and detecting Alloiococcus otitidis. The present invention.

Expression the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28
treating and diagnosing diseases, drug screening assays and monitoring effects during drug clinical trials.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            119 TGGGCTACCACCTTTTAATGGCTAACCCCTTCCGCCTGAACGACGGCTGGGCCAAGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     922 GAGCGCTTGCGATCCTCGCTTCCGGCGATCCGGGAGCGGTGATTGAAGCGATCGAGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             688 TCGTAAAAGGGACGATTGATTATGTATCGCCCCAATATATTGTCATTGAAAACGGCGGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               802 AAACAATCTATACATACCATTATGTAAGAGAAGACACGAATGCGCTGTACGGCTTTTCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAAGGGAAGAAAAATGCTGTTTACGAAAATGCTGAATGTTACGGGGATCGGCCCAAAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 TITATCTGTGGTATAATAAATGACTATTGGAAAAAGTGGTGAAAGTA---TGTATGAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              748 TCGGCTATCAGATCTTCACGCCAAATCCGTTTATTATAAGAAAA----ACAGCAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 654;
                                                                                                                                                                                                        present invention describes an isolated polynucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 654 BP; 192 A; 148 C; 155 G; 159 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9.9%; Score 104.8; DB 9;
56.0%; Pred. No. 3.3e-21;
tive 0; Mismatches 182;
                                                                                                                     Claim 7; SEQ ID NO 5563; 1019pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 56.0 Matches 243; Conservative
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982 AGGACGAAGCATTTCTCGTCAAATTTCCCGGCGTAGGCAAAAAAACGGCAAGGCAGATCA 1041

rrcrecaccrcada 432

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                                                                                                                                                                              ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading frame (ORF) nucleic acid sequences which encode the amino acid sequences given in ABPS3124 to ABP37960. The S. epidermidis sequences have antibacterial activity and can be used in gene therapy. The sequences can also be used in the diagnosis and treatment of bacterial infections, particularly S. epidermidis infections. The sequences can be used to screen for compounds able to interfere with the S. epidermidis life cycle or inhibit S. epidermidis infection. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained
                                                                                                                                     epidermidis; open reading frame; ORF; bacterial infection; gene therapy; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       679 TGATCGAATTCGTAAAAGGGACGATTGATTATGTATCGCCCCAATATATTGTCATTGAAA 738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   254 GACCTAAATCAGCTTTAGCGATACTTGCTTCAAGTACACCACATGAAGTTAAATTGGCTA 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            739 ACGGCGGGATCGCCTATCAGATCTTCACGCCAAATCCGTTTATTATAAGAAAAAACAGCA 798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74 CATGTGGCATAGGTTATGAGATACAAACGCCTAATTCCTATCGTTTTCAAAAATATCTTG 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAGAAACAATC----TATACATACCATTATGTAAGAGAAGACACGAATGCGCTGTACG 852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    134 AAAAAGAAGTCCAAATTTATATACTTCACTAATTGTACGAGAAGATGCTCAACTACTATATG 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        853 GCTTTTCGACAAGGGAAGAAAAATGCTGTTTACGAAAATGCTGAATGTTACGGGGATCG 912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       194 GCTTTATTAATGAAGAAGAAAAAAATGTTTCTTAGCTTAATAAAAGTGACTGGGATAG 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              913 GCCCAAAAGGAGCGCTTGCGATCCTCGCTTCCGGCGATCCGGGAGCGGTGATTGAAGCGA 972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14 TGTATGCATATATTAAAGGAACATTATCTCAGTTGTTCCCTACACATGTAGTGGTTGAGA 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel isolated nucleic acid encoding a Staphylococcus epidermis polypeptide, useful for diagnosing and treating bacterial infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Staphylococcus epidermidis ORF nucleic acid sequence SEQ ID NO:780.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 615 BP; 241 A; 90 C; 110 G; 174 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            in electronic format directly from the USPTO web site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9.8%; Score 103.4; DB 6; 56.4%; Pred. No. 8.6e-21; iive 0; Mismatches 161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; SEQ ID NO 780; 267pp; English.
                                                                                                                                                                                                                                                                                                                                                                                            (GENO-) GENOME THERAPEUTICS CORP.
ABN91317 standard; DNA; 615 BP
                                                                                                                                                                                                                                                                                                                                      97US-0055779P.
97US-0064964P.
                                                                                                                                                                                                                                                                                                     98US-00134001
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                                                                                                                                                                                           Staphylococcus epidermidis
                                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Doucette-Stamm LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P-PSDB; ABP38772
                                                                                                                                                            antibacterial;
                                                                                                                                         Staphylococcus
                                                                                                                                                                                                                                US6380370-B1
                                                                                                                                                                                                                                                                                                     13-AUG-1998;
                                                                                                                                                                                                                                                                                                                                        14-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                         08-NOV-1997;
                                                                                                                                                                                                                                                                  30-APR-2002.
                                                                    24-JUL-2002
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The invention describes an isolated nucleic acid comprising a nucleotide sequence with any of 3772 fully defined nucleotide sequences (SEQ ID NO: 1-3772) and encoding an Staphylococcus epidermidis polypeptide with any of 3772-7544) as given in the specification. Also described are: a recombinant expression vector; a cell comprising a recombinant expression vector of (1); producing an S. epidermidis polypeptide; an isolated nucleic acid comprising a nucleotide sequence of at least 8 nucleotides in length; a vaccine composition for prevention or treatment of an S. epidermidis infection, comprising a nucleic acid cited above and a carrier; treating a subject for S. epidermidis infection; a recombinant or substantially controlly preparation of an S. epidermidis polypeptide or its fragment; a subject for S. epidermidis infection; a recombinant or substantially concens composition of an S. epidermidis polypeptide or its fragment; a subject for sequence of a Staphylococcus succided in a sample; a computer readable medium having recorded in it the nucleotide sequence with SEQ ID NO: 1-3772 or its fragments; a computer based system for identifying fragments of the Staphylococcus genome of commercially importance; a computer based system for identifying fragments of the Staphylococcus genome and/or plasmids; and identifying an expression modulating fragment of the Staphylococcus genome and/or plasmids; and identifying an expression modulating fragment compositions of the present invention are useful for the diagnosis, prevention and/or treatment of an Staphylococcus epidermidis bacterial confection. This sequence encodes a S. epidermids protein of the invention.
antibacterial; vaccine; antisense therapy; Staphylococcus epidermidis; recombinant expression vector; infection; computer readable medium; computer based system; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated polypeptide and encoding nucleic acid derived from Staphylococcus epidermidis, useful for diagnosing, preventing and/or treating an S. epidermidis bacterial infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Staphylococcus epidermis polynucleotide seqid 364.
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                                                                                   GGCAGATCATCCTTGACCTGAAA 1055
                                                                                                                                                                  374 GACAATTGTGTTAGATTTAAAA 396
                                                                                                                                                                                                                                                                                                                                                                                 ВP.
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98US-00134001.
99US-00450969.
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                                                                                                                                                                                                                                                                                                                                                                                 ADS01069 standard; DNA; 615
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bush
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13-AUG-1998;
29-NOV-1999;
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                                                                        679 TGATCGAATTCGTAAAAGGGACGATTGATTATGTATCGCCCCAATATATTGTCATTGAAA
                                                                                                retaticcatatataaaggaacattatcicagtrefrectacacateragregaga
                                                                                                                                                 CATGTGGCATAGGTTATGAGATACAAACGCCTAATTCCTATCGTTTTCAAAAATATCTTG
                                                                                                                                                                          AAGAAACAATC-----TATACATACCATTATGTAAGAGAAGACACGAATGCGCTGTACG
                                                                                                                                                                                                                           GCTTTTCGACAAGGGAAGAAAAATGCTGTTTACGAAAATGCTGAATGTTACGGGGATCG
                                                                                                                                                                                                                                                  GCTTTATTAATGAAGAGGAAAAGAAATGTTTCTTAGCTTAATAAAAGTGACTGGGATAG
                                                                                                                                                                                                                                                                           GCCCAAAAGGAGCGCTTGCGATCCTCGCTTCCGGCGATCCGGGAGCGGTGATTGAAGCGA
                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New Straptococcus pneumoniae polynucleotides, useful for treating o preventing S. pneumoniae infections, or non-systemic diseases, e.g. otitis media, which are induced or exacerbated by S. pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptococcus pneumoniae; infection; otitis media; antibacterial;
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П
                         Length 615;
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A; 90 C; 110 G; 174 T; 0 U; 0 Other;
                                                 Indels
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                        DB 13;
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                                    Pred. No. 8.6e-21;
0; Mismatches 161;
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                       9.8%; Score 103.4; 56.4%; Pred. No. 8.6
                                                                                                                                                                                                                                                                                                                                                                           GGCAGATCATCCTTGACCTGAAA 1055
                                                                                                                                                                                                                                                                                                                                                                                                  GACAAATTGTGTTAGATTTAAAA 396
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              diagnosis; gene therapy; gene; ds
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18-APR-2001; 2001US-0284443P.
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                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptococcus pneumoniae
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 BP; 241
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P-PSDB; ABP81305.
                                    Similarity
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Sequence 615
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-MAR-2003
                                                216;
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                        Query Match
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GCGATCGAGAATGAGGACGAAGCATTTCTCGTCAAATTTCCCGGCGCTAGGCAAAAAAAGG 1028
                a Streptococcus pneumoniae genomic sequence, a fragment or degenerate variant of the polynucleotide or a nucleic acid sequence 95% identical to one of the polynucleotides. The S. pneumoniae polynucleotides and encoded polypeptides (ABPB1299-ABPB1674) are useful for treating or preventing S. pneumoniae infections or non-systemic diseases, e.g. otitis media, which are induced or exacerbated by S. pneumoniae. These are also useful for detecting S. pneumoniae in a biological sample or disgnosing S. pneumoniae in a biological sample or disgnosing S. pneumoniae in gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            252
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                                                                                                                                                                                                                                                                                                                                                                                   72
                                                                                                                                                                                                                                                                                                                                                                                                                           735 GAAAACGGCGGGATCGGCTAT-----CAGATCTTCACGCCAAATCCGTTTATTATAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          189 AAAAACAGCAAAGAAACAATCTATACATACCATTATGTAAGAGAGACACGAATGCGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             253 ATTGGTCCTGTATCAGCTCTTGCTATTATCGCTGCTGATGACAATGCTGGCTTGGTTCAA
  invention relates to isolated polynucleotides (ABZ72147-ABZ42522)
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                                                                                                                                                                                                                                                               Length 609;
                                                                                                                                                                                                                          Sequence 609 BP; 184 A; 119 C; 146 G; 160 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                             Score 89.8; DB 8; Length 6
Pred. No. 1.3e-16;
0; Mismatches 172; Indels
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Sequence 1, Application US/10510408
Publication No. US20050221423A1
GENERAL INFORMATION:
APPLICANT: Orgeneen, Steen Troels
APPLICANT: Andereen, Jens Tonne
APPLICANT: Ranuesen, Michael Dolberg
TITLE OF INVENTION: Improved Bacillus Host Cell
FIRE REPERENCE: 10295.204-US
CURRENT APPLICATION NUMBER: US/10/510,408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 191
SOFTWARE: PatentIn version 3.3
SEQ ID NO 1
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                                                                                                                                  February 27, 2006, 06:32:27; Search time 1034 Seconds (without alignments) 8437.325 Million cell updates/sec
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2: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
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9: /cgn2_6/ptodata/1/pubpna/USO9B_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/USO9B_PUBCOMB.seq:*
5.1.7
Biocceleration Ltd.
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GenCore version
Copyright (c) 1993 - 2006
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Maximum Match 100%
Listing first 45 summaries
                                                                                          - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No. 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	SCORE 109459 10055 11004 1122 1122 1104 1104 1104 1104 110	Match Match 100.0 111.6 113.0 111.6 101.3	Advantage of the control of the cont	# 6 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	ID	Sequence 1, Appli Sequence 3090, Ap Sequence 5972, Ap Sequence 5972, Ap Sequence 5561, App Sequence 7, Appli Sequence 40, Appli Sequence 40, Appli Sequence 40, Appli Sequence 302, App Sequence 311, App Sequence
21 22 23	84.8 65.6 61.4	5.60	2121 10996 45613	737	US-10-398-221-3601 US-09-070-927A-202 US-10-672-787-22	Sequence 3601, Ap Sequence 202, App Sequence 22, Appl

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Gaps

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Length 1055; Indels

100.0%; Score 1055; DB 9; ilarity 100.0%; Pred. No. 3.6e-304; Conservative 0; Mismatches 0;

Similarity

Query Match Best Local Simi Matches 1055;

TYPE: DNA ORGANISM: Bacillus licheniformis

LENGTH: 1055

NAME/KEY: CDS LOCATION: (34)..(552)

FEATURE:

US-10-510-408-1

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121 GAAAAGCCGGCTAAAGTTCAAATCCAGCTTGAAAAGGTTTATCTGGACGGAGACGTTGGA 181 ATTGAGAATAAAGTAGAGGCCGCTCGCACACTGGAAGACTTTAAAAGCTGCTTATAAAGGG

GAAAAGCCGGCTAAAGTTCAAATCCAGCTTGAAAAGGTTTAATCTGGACGAGACGTTGGA

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TGGCAGCTCATCGATCAGAAAAGGGGTTTATTCTGTTTCGCAAACAGGTGGACGACATT 300

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Sequence 1, Appli	Sequence 6812, Ap	Sequence 1, Appli	Sequence 573, App	Sequence 684, App	Sequence 960, App	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 7048, Ap	Sequence 2571, Ap	Sequence 2570, Ap	Sequence 2572, Ap	Sequence 16, Appl	Sequence 1068, Ap	Sequence 6822, Ap	Sequence 102700,	Sequence 102701,	Sequence 3546, Ap	Sequence 1, Appli	Sequence 5571, Ap	Sequence 117840,
US-10-470-565-1	6 US-10-156-761-6812	US-10-156-761-1	US-10-795-159-573	US-10-795-159-684	US-10-194-163-960	US-10-329-670-1	US-10-158-865-1	US-10-981-687-1	US-10-719-993-7048	US-10-335-977-2571	US-10-335-977-2570	US-10-335-977-2572	US-10-915-740A-16	US-10-915-740A-1068	US-10-719-993-6822	US-09-925-065A-102700	US-09-925-065A-102701	US-10-739-930-3546	US-10-312-841-1	US-10-501-282-5571	US-10-424-599-117840
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                                                                                                                                                 43.5%; Score 459; DB 3; Le
100.0%; Pred. No. 3.7e-126;
ive 0; Mismatches 0;
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85.5%; Pred. No. 2.7e-47;
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Fatent No. US20020146721A1
GENERAL INFORMATION:
APPLICANT: Berka, Randy M.
TITLE OF INVENTION: Methods For Monitoring Mul;
TITLE OF INVENTION: Expression
TITLE OF INVENTION: Expression
FILIE REFERENCE: 10085.500-US
CURRENT APPLICATION NUMBER: US/09/974,300
CURRENT FILING DATE: 2001-10-05
FRIOR FILING DATE: 2000-10-06
FRIOR FILING DATE: 2000-06
FRIOR FILING DATE: 2000-03.27
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SOFWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1616
LENGTH: 546
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                     LENGTH: 459
TYPE: DNA
ORGANISM: Bacillus licheniformis
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LOCATION: (1)...(546)
CTHER INFORMATION: n = A,T,C
US-09-974-300-1616
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Best Local Similarity 100.(
Matches 459; Conservative
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Best Local Similarity
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US-09-974-300-1616
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SEQ ID NO 3090
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                                                                               TCTCCCCTCAGCAAACAAACGGTTATATCGGAGTGACTGAAGATGGCGTGATTTCGACT
                                                                                                                                                                              TTTCACGGTCGCCCGGGCATCTTATCAGAACCCATTCAATCGTTTTTTCAGGATTGATATA
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                                               TCTCCCCTCAGCAAAACAAACGGTTATATCGGAGTGACTGAAGATGGCGTGATTTCGACT
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; Sequence 3090. Application US/09974300
; Patent No. US20020146721A1
; GENERAL INFORMATION:
; APPLICANT: Berka, Randy M.;
; APPLICANT: Clausen, Ib Groth
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
; TITLE OF INVENTION: Expression
; FILE REPRENCE: 10085.500-US
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 05/60,598
; PRIOR PELING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/279,526
; PRIOR PELING DATE: 2000-10-06
; PRIOR PELING DATE: 2000-10-06
; PRIOR FILING DATE: 2000-10-06
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                                                                                                                                                                                          Sequence 8, Application US/1039821
| Publication No. US20040018514A1
| GENERAL INFORMATION:
| APPLICANT: GLASER, Philippe
| TILE OF INVENTOR: Listeria innocua, genome and applications
| TILE OF INVENTOR: US/10/398,221
| CURRENT APPLICATION NUMBER: US/10/398,221
| CURRENT APPLICATION NUMBER: PCT/FR 01/03 061
| PRIOR PILING DATE: 2003-03-27
| PRIOR FILING DATE: 2001-10-04
| PRIOR FILING DATE: 2000-10-04
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| LOCATION: (1)..(end)
| OTHER INFORMATION: n can be any nucleotide: a, g, US-10-398-211-8
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Pred. No. 1.1e-23;
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; Publication No. US20040018514A1
; APPLICANT: KUNST, Frederik
                                                1033 GGCAGATCATCCTTGACCTGAAA
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59.4%;
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                                           766 CGCCAAATCCGTTTATTATAAGAAAACAGCAAAGAAACAATCTATACATA---CCATT
                                                                                                                                                                                                                                                              147 TTTACGAAATGCTGAATGTTACGGGGATCGGCCCAAAAGGAGCGCTGCCGATCCTCGCT
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; Sequence 5972, Application US/09974300
; Patent No. US202020146721A1
; GENERAL INFORMATION:
; APPLICANT: Clausen, Ib Groth
; TITLE OF INVENTION: Expression
; TITLE OF INVENTION: Berpession
; FILE REFREEDER 10085.500-US
; CURRENT APPLICATION NUMBER: US/09/974,300
; CURRENT PILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 09/680,598
; PRIOR PILING DATE: 2000-10-06
; PRIOR PILING DATE: 2000-10-06
; PRIOR PILING DATE: 2001-03-07
; WUMBER OF SEQ ID NOS: 8481
; SOFTWARE: FastSEQ for Windows Version 4.0
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Pred. No. 8.1e-30;
0; Mismatches 140; Indels
  IndelB
  37;
  0; Mismatches
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Best Local Similarity 61.9%;
Matches 237; Conservative
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US-09-974-300-5972
253; Conservative
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; TYPE: DNA
; ORGANISM: Alloiococcus otitidis
US-10-501-282-6651
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                                                                                                         10.3%;
best Local Similarity 56.3%;
Matches 247; Conservative
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; LOCATION: (49)
US-10-501-282-5561
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      LENGTH:
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APPLICANT: RUSSELL, DAVID PARRISH
APPLICANT: RUSSELL, DAVID PARRISH
TITLE OF INVENTION: ALLOIOCOCCUS OTITIDIS OPEN READING FRAMES (ORFS) ENCODING
TITLE OF INVENTION: POLYPEPTIDE ANTIGENS, IMMUNOGENIC COMPOSITIONS AND USES THEREOF
FILE REFERENCE: ANION'80 L2
CURRENT APPLICATION NUMBER: US/10/501,282
CURRENT PILING DATE: 2004-07-09
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## APPLICANT: GLASER, Philippe
### TITLE OF INVENTION: Listeria innocua, genome and applications
### FILE REFERENCE: 344 702 - US
### FILE REFERENCE: 344 702 - US
### CURRENT APPLICATION NUMBER: US
### CURRENT FILING DATE: 2003-03-27
### PRIOR APPLICATION NUMBER: PCT/FR 01/03 061
### PRIOR APPLICATION NUMBER: FR 00/12 697
### PRIOR APPLICATION NUMBER: FR 00/12 697
### NUMBER OF SEQ ID NOS: 4025
### NUMBER OF SEQ ID NOS: 4025
### SEQ ID NO 2058
### LENGTH: 3011208
                                                                                                                                                                                                                                                                                                                                                                                      Length 3011208
                                                                                                                                                                                                                                                                                                                                                                                    11.6%; Score 122; DB 7; Length 30
59.4%; Pred. No. 3.2e-23;
ive 0; Mismatches 150; Indels
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PRIOR FILING DATE: 2001-11-29
PRIOR PILING DATE: 2001-11-29
PRIOR PILING DATE: 2002-11-18
PRIOR FILING DATE: 2002-11-18
PRIOR PILING DATE: 2002-11-25
NUMBER: PCT/USO2/36123
NUMBER: PCT/USO2/36123
SEQ ID NO 6651
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                                                                                                                                                                                                                                                                                            ; TYPE: DNA; Cisteria innocua
GS-10-398-221-2058
                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 59.4
Matches 228; Conservative
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APPLICANT: ZAGURGKY, ROBERT JOHN
APPLICANT: RUSSELL, DAVID PARRISH
APPLICANT: RUSSELL, DAVID PARRISH
APPLICANT: RUSSELL, DAVID PARRISH
APPLICANT: RUSSELL, DAVID PARRISH
TITLE OF INVENTION: ALLOIOCOCCUS OTITIDIS OPEN READING FRAMES (ORFS) ENCODING
TITLE OF INVENTION: POLYPEPTIDE ANTIGENS, IMMUNOGENIC COMPOSITIONS AND USES THEREOF
FILE REPERENCE: AMNO180 L2
CURRENT APPLICATION NUMBER: US/10/501,282
CURRENT FILING DATE: 2004-07-09
PRIOR FILING DATE: 2004-11-29
RIOR APPLICATION NUMBER: 60/426,742
PRIOR APPLICATION NUMBER: FOTYUSO2/36123
PRIOR FILING DATE: 2002-11-25
PRIOR FILING DATE: 2002-11-25
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                                                                                 Gaps
                                                                                 Indels
Score 108.2; DB 9;
Pred. No. 3.1e-19;
0; Mismatches 183;
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APPLICANT: MCMICHAEL, JOHN CALHOUN
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/10/724,972A
CURRENT FILING DATE: 1999-11-29
PRIOR FILING DATE: 1999-11-29
PRIOR FILING DATE: 1999-11-39
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 7544
SEQ ID NO 364
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                 2 TITATCIGIGGTATAATAAAAGACTATIGGAAAAAGGGGGGAAAAGTA.--TGTAIGAAT
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Pred. No. 9.2e-20;
0; Mismatches 161;
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Publication No. US20040147734A1
GENERAL INFORMATION:
APPLICANT: Doucette-Stamm, Lynn
APPLICANT: Bush, David
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Best Local Similarity 56.4%;
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US-10-724-972A-364
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Sequence 5563, Application US/10501282

Publication No. US20050203280A1

GENERAL INFORMATION:

APPLICANT: MCMICIAEL, JOHN CALHOUN

APPLICANT: RUSSELL, DAVID PARRISH

TITLE OF INVENTION: PLETCHER, LEAH DIANS

TITLE OF INVENTION: PLOYPEPTIDE ANTIGENS, IMMUNGENIC COMPOSITIONS AND USES THEREOF

FILE REFERENCE: AM100780 L2

CURRENT APPLICATION NUMBER: 60/426,742

PRIOR FILING DATE: 2004-11-29

PRIOR FILING DATE: 2002-11-18

PRIOR PILING DATE: 2002-11-25

NUMBER OF SEQ ID NOS: 6653

SOFTWARE: PATCHIN VERSION 3.2

SEQ ID NO 5563

LENGTH: 654
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                 Length 654;
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     Score 104.8; DB 9;
Pred. No. 3.6e-20;
0; Mismatches 182;
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cch 9.9%;
al Similarity 56.0%;
243; Conservative (
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; LOCATION: (22).
US-10-501-282-5563
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     Query Match
Best Local S
Matches 243
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Sequence 40, Application US/08961527

Publication No. US20020032323A1

GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
NUMBER OF SEQUENCES: 391

CORRESPONDENCE ADDRESS:
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8.5%; Score 89.8; DB 2; Length 1.
Best Local Similarity 54.0%; Pred. No. 6.4e-15;
Matches 209; Conservative 0; Mismatches 172; Indels
                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS Version 6.2
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                                                                                                                                                                                   ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue CITY: Rockville STATE: Maryland COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: PB3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 14273 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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STRANDEDNESS: double
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CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                              20850
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Publication No. US20040110181A1
GENERAL INFORMATION:
APPLICANT: Wyeth
TITLE OF INVENTION: ANTIGENS AND USES THEREOF
FILE REFERENCE: AMTIGENS AND USES THEREOF
FILE REFERENCE: AMTO645-PCT
CURRENT APPLICATION NUMBER: US/10/474,776
CURRENT FILING DATE: 2003-10-14
NUMBER OF SEQ ID NOS: 752
SOFTWARE: Patentin version 3.1
SEQ ID NO 7.
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                                                                                                                194 GCTTTATTAATGAAGAAGAAAAAGAAATGTTTCTTAGCTTAATAAAAGTGACTGGGATAG 253
                                                                                                                                                                 GCCCAAAAGGAGCGCTTGCGATCCTCGCTTCCGGCGATCCGGGAGCGCTGATTGAAGCGA 972
                                                                                                                                                                                                               254 GACCTAAATCAGCTTTAGCGATACTTGCTTCAAGTACACCACATGAAGTTAAATTGGCTA 313
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                 134 AAAAAGAAGTCCAAATTTATACTTCACTAATTGTACGAGAAGATGCTCAACTACTATATG 193
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                                                                  GCTTTTCGACAAGGGAAGAAAAATGCTGTTTACGAAAATGCTGAATGTTACGGGGATCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8.5%; Score 89.8; DB 7; 54.0%; Pred. No. 1.1e-15;
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ORGANISM: Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 54.09
Matches 209; Conservative
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US-08-961-527-40
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SEQ ID NO 4979
LENGTH: 2162598
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                                                              APPLICANT: Kunsch et al.
TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
NUMBER OF SEQUENCES: 391
CORRESPONDENCE ADDRESS:
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                                                                                                                                                       ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: CD-R
COMPUTER: Dell Latitude Pentium 3
OPERATING SYSTEM: Windows 98
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/158,844
FILING DATE: 03-Unn-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION NUMBER: US 08/961,527
FILING DATE: 1997-10-30
APPLICATION NUMBER: US 08/961,527
FILING DATE: 1997-10-10
APPLICATION NUMBER: US 06/029,960
FILING DATE: 1996-10-31
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Hyman, Mark J.
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB340P1D1
INFORMATION FOR SEQ ID NO: 40:
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Sequence 40, Application US/10158844 Publication No. US20040029118A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 14273 base pairs
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STRANDEDNESS: double
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                                                                                                                                                                                                                                                                   ZIP: 20850
COMPUTER READABLE FORM:
                                                                                                                                                                                                   CITY: Rockville STATE: Maryland
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nes 209; Conserv
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Matches
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65596 GAAACCAATGGTATTGGTTATATCTGCATGTGGCCAATCCTTATGCCTATTCAGGTCAG 65655
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Sequence 4979, Application US/10472928
Publication No. US20050020813A1
GENERAL INFORMATION:
APPLICANT: THE INSTITUTE FOR GENOMIC RESEARCH
TITLE OF INVERTION: STREPFOCOCCUS PNEUMONIAE PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE: P026926W0
CURRENT APPLICATION NUMBER: US/10/472,928
CURRENT PILING DATE: 2003-09-26
PRIOR APPLICATION NUMBER: GB-0107658.7
PRIOR APPLICATION NUMBER: GB-0107658.7
SPRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 4979
SOFTWARE: SeqMin99, version 1.03
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Publication No. US20050020813A1
GENERAL INFORMATION:
APPLICANT: CHIRON SPA
TITLE OF INVENTION: STREPFOCOCCUS PNEUMONIAE PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE: PO26926W0
CURRENT APPLICATION NUMBER: US/10/472,928
CURRENT FILING DATE: 2003-09-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               65536 ACTATGTACGCATATTTAAAAGGAATCATTACCAAAATTACTGCCAAATACATTGTTCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       735 GAAAACGGCGGGATCGGCTAT-----CAGATCTTCACGCCAAATCCGTTTATTATAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 89.8; DB 8;
Pred. No. 1.1e-13;
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PRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 4979
SOFTWARE: Seqwin99, version 1.03
SEQ ID NO 167
LENGTH: 591
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Best Local Similarity 54.0
Matches 209; Conservative
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973 TCGAGAATGAGGACGAAGCATTTCTCGTCAAATTTCCCGGCGTAGGCAAAAAAACGGCAA 1032
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                                                                                                                                                                                                                                      739 ACGGCGGGATCGCCTAT-----CAGATCTTCACGCCAAATCCGTTTATTATAAGAAAA 792
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                                                                                                                      Gape
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                                                                             Query Match 8.4%; Score 89; DB 8; Length 591; Best Local Similarity 54.0%; Pred. No. 1.8e-15; Matches 207; Conservative 0; Mismatches 170; Indels
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Search completed: February 27, 2006, 08:12:58 Job time : 1047 secs

Sequence 524053, Sequence 124018, Sequence 108779, Sequence 42643, A Sequence 42643, A Sequence 12675, A Sequence 13473, A Sequence 601441, Sequence 5026, Ap

8 US-10-750-623-32606 6 US-09-925-065A-29480 6 US-09-925-065A-29480 6 US-09-925-065A-410936 6 US-09-925-065A-486702 6 US-09-925-065A-486702 6 US-09-925-065A-486703 6 US-09-925-065A-11112-08-65 1 US-11-112-08-65 6 US-09-925-065A-12413 6 US-09-925-065A-12413 6 US-09-925-065A-12413 6 US-09-925-065A-12413 6 US-09-925-065A-12413 12 US-11-114-36A-12642 6 US-09-925-065A-12413 6 US-09-925-065A-12413 6 US-09-925-065A-13473 6 US-09-925-065A-313709 6 US-09-925-065A-313709 8 US-10-995-065A-313709 8 US-10-995-065A-313709 8 US-09-925-065A-313709 8 US-09-925-065A-313709 8 US-09-925-065A-313709 8 US-09-925-065A-313709 8 US-09-925-065A-313709

525 100000 394468

Sequence 65, Appl Sequence 211, Ap

Sequence 295480, Sequence 410936, Sequence 503465, Sequence 486701, Sequence 486702, Sequence 701231,

Sequence 247578, Sequence 333708, Sequence 333708, Sequence 333709, Sequence 13378, A Sequence 268787,

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Sequence 8739, Ap
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Sequence 2695, Ap
Sequence 6709, Ap
                                                                                                                                                          February 27, 2006, 06:31:38; Search time 939 Seconds (without alignments) 2395.790 Million cell updates/sec
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1: /cgn2_6/ptodata/1/pubpna/USOB NEW PUB.seq:*

2: /cgn2_6/ptodata/1/pubpna/USOB_NEW_PUB.seq:*

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                    GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd
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US-09-925-065A-102700

US-09-925-065A-102701

US-09-925-065A-295479

US-09-925-065A-295479

US-09-925-065A-295479

US-09-925-065A-174583

US-09-925-065A-17413

US-09-925-065A-17413

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US-10-467-657-2695
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2 US-11-098-686-10086
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Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Clausen, ID Groth
APPLICANT: Olsen, Peter Bjarke
APPLICANT: Olsen, Peter Bjarke
APPLICANT: Olsen, Peter Bjarke
APPLICANT: Rasmussen, Michael Dolberg
TITLE OF INVENTION: Improved Bacillus Host Cell
FILE REFERENCE: 10294.204-US
CURRENT APPLICATION NUMBER: US/10/510,386
CURRENT FILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 248
SOFTWARE: Patentin version 3.3
SEQ ID NO 123
FILE TITLE OF THE TITLE OF
ALIGNMENTS
                                                                                                                                     US-10-510-386-123
Sequence 123, Application US/10510386
Publication No. US20050244922A1
GENERAL INFORMATION:
APPLICANT: Andersen, Jens Tonne
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ORGANISM: Bacillus licheniformis
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US-10-510-386-123
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Length 612;

Score 48.8; DB 8; Pred. No. 0.0032; 0; Mismatches 127;

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PRIOR APPLICATION NUMBER: GB-0103424.8
PRIOR FILING DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 9218
SOFTWARE: SeGWin99, version 1.04
SEQ ID NO 2655
LENGTH: 612
                                                                                           ; TYPE: DNA
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-2695
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Best Local Similarity 49.6
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   ATTGAGAATAAAGTAGAGGCCGCTCGCACACTGGAAGACTTTAAAGCTGCTTATAAAGGG 707
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                                                                                               TCTCCCCTCAGCAAACAAACGGTTATATCGGAGTGACTGAAGATGGCGTGATTTCGACT
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Sequence 6709, Application US/10467657

Publication No. US20050260581A1

GENERAL INFORMATION:
APPLICANT: CHIRON SPA
APPLICANT: FOUTANA MARIAR Rita
APPLICANT: MASIGNANI Vega
APPLICANT: MASIGNANI Vega
APPLICANT: MASIGNANI Vega
APPLICANT: MASIGNANI Vega
APPLICANT: MONACI Blisabetta
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE:
CURRENT PILLING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: GB-0103424.8
PRIOR FILING DATE: 2001-02-12
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49.6%; Pred. No. 0.0032;
tive 0; Mismatches 127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: DNA
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-6709
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SEQ ID NO 6709
GrcrrccaAcrc 414
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APPLICANT: CHIRINON SpA
APPLICANT: CHIRINON SpA
APPLICANT: FONTANA Maria Rita
APPLICANT: PASZA Mariagrazia
APPLICANT: MASIGNANI Vega
APPLICANT: MONACI Blisabetta
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
TILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/467,657
CURRENT FILING DATE: 2003-08-11

Sequence 2695, Application US/10467657 Publication No. US20050260581A1 GENERAL INFORMATION:

US-10-467-657-2695

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785 TAAGAAAAACAAGAAACAATCTATACATACCATTATGTAAGAGAGACACGAATGC 844
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TITLE OF INVENTION: NUCLEIC ACID AND POLYPERTIDE SEQUENCES
TITLE OF INVENTION: FROM LAWSONIA INTRACELLULARIS AND METHODS OF USING
FILE REFERENCE: 09531-128001
CURRENT APPLICATION NUMBER: US/11/098,686
CURRENT FILING DATE: 2005-04-04
PRIOR PILING DATE: 2005-01-01
PRIOR PAPLICATION NUMBER: US 60/416,395
PRIOR PILING DATE: 2002-10-01
PRIOR PILING DATE: 2002-10-04
NUMBER OF SEQ ID NOS: 11433
SOFTWARE: PRASEQ for Windows Version 4.0
SEQ ID NO 10086
LENGTH: 600
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Publication No. US20060024696A1
GENERAL INFORMATION:
APPLICANT: Kapur, Vivek and Gebhart, Connie J.
TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES
TITLE OF INVENTION: FROM LAWSONIA INTRACELLULARIS AND METHODS OF USING
FILE REFERENCE: 09531-12801
CURRENT APPLICATION NUMBER: US/11/098,686
PRIOR APPLICATION NUMBER: PCT/US03/31318
PRIOR RILING DATE: 2003-10-01
PRIOR FILING DATE: 2003-10-01
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Publication No. US20060024696A1
GENERAL INFORMATION:
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TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108877.132
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR PILING DATE: 2000-10-24
PRIOR PILING DATE: 2000-11-20
PRIOR FILING DATE: 2000-11-30
PRIOR FILING DATE: 2000-11-30
PRIOR FILING DATE: 2000-11-30
PRIOR FILING DATE: 2001-01-130
PRIOR FILING DATE: 2001-01-16
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PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
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50.5%; Pred. No. 1.7;
ive 0; Mismatches
PRIOR FILING DATE: 2002-10-04
NUMBER OF SEQ ID NOS: 11433
SOFTWARE: FastSEQ for Windows Version 4.0
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 102700
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                                                                                                                                   TYPE: DNA
ORGANISM: Lawsonia intracellularis
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US-09-925-065A-102700
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US-09-925-065A-102700/c
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Best Local Similarity
                                                                          SEO ID NO 8739
LENGTH: 1457619
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Publication No. US20050255478A1
GENERAL INFORMATION
APPLICANT: KIMMERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REPERENCE: PUB48002
CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT FILING DATE: 2004-03-04
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Gaps
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GENERAL INVENTION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REPERENCE: 108827.135

CURRENT APPLICATION NUMBER: US/09/925.065A

CURRENT FILING DATE: 2001-08-08

PRIOR APPLICATION NUMBER: US 60/243,096

PRIOR APPLICATION NUMBER: US 60/252,147

PRIOR APPLICATION NUMBER: US 60/250,092

PRIOR FILING DATE: 2000-11-30

PRIOR FILING DATE: 2000-11-30

PRIOR PRILING DATE: 2001-01-16

PRIOR PRILING DATE: 2001-01-16

PRIOR PRILING DATE: 2001-01-16

PRIOR PLILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-00-16

SEQ ID NO 102701

LENGTH: 636
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; Pred. No. 1.7;
0; Mismatches
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; Sequence 102701, Application US/09925065A
; Publication No. US20040181048A1
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PRIOR APPLICATION NUMBER: 60/164,258
PRIOR FILING DATE: 1999-11-09
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Best Local Similarity 50.5%;
Matches 94; Conservative
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US-09-925-065A-102701
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459 AACTTTTGGTAAAATATGTTATTTATTTAACATGTAAATGTTTTATGATTGTTATTTT 400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 295479, Application US/09925065A

Sequence 295479, Application US/09925065A

Publication No. US20040181048A1

GENERAL INFORMATION:
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
TITLE OF INVENTION: NUMBER: US/09/925,065A

CURRENT FILING DATE: 2001-08-08

PRIOR APPLICATION NUMBER: US 60/243,096

PRIOR APPLICATION NUMBER: US 60/252,147

PRIOR APPLICATION NUMBER: US 60/250,092

PRIOR APPLICATION NUMBER: US 60/261,766

PRIOR PRILING DATE: 2001-01-30

PRIOR PILING DATE: 2001-01-30

PRIOR PILING DATE: 2001-01-30

PRIOR PILING DATE: 2001-01-30

PRIOR PILING DATE: 2001-01-30

PRIOR PILING DATE: 2001-01-30

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PRIOR PILING DATE: 2001-01-30

PRIOR PILING DATE: 2001-01-30

PRIOR PILING DATE: 2001-01-30

PRIOR PILING DATE: 2001-01-30

PRIOR PILING DATE: 2001-05-09

NUMBER OF SEQ ID NOS: 957066

SOFTWARE: PRESEQ for Windows Version 4.0

LEMNTH: 6.44
                                                                                                                                                                                                           CTHER INFORMATION: Description of Artificial Sequence: synthetic; CTHER INFORMATION: nucleic acid sequence
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                                                                                                                                                                                                                                                                                                                                          DB 8; Length 2436;
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                                                                                                                                                                                                                                                                                                                                       Score 37.6; DE
Pred. No. 6.3;
0; Mismatches
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65.5%;
                                                                                                                               TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity 48.1
Matches 101; Conservative
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4398
LENGTH: 2436
                                                                                                                                                                                                                                                                                                                                                                                                         55; Conservative
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US-09-925-065A-295479
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Best Local Similarity
Matches 55; Conservi
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US-09-925-065A-295479/c
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572 TTCAGCTGCAGACAGAAGCTTTTTAGCGAACATATGTTAACTTTTTCATTCTAGCTTTG 631
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                                                                   358 GGAAAAACATTTATAAGAAGTCAGCTTATGGTTAGAAGTCAGCTTAATGAAAAGATGATAT
GAAAAAGGAATTTGAACATGTCATTGAAGCCGTAAAATCATCCGGAAGCCAACATGT
                                                                                                                                                       537 AGAAGATATGAAGACATGACGCTGTTATGTCTTTTTTCAGCTGCAG--ACAGAAGCTTTT
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US-09-925-065A-147413/C
is Sequence 147413, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
i APPLICANT: Wang, David G.
i TITLE OF INVENTION: Identification and Mapping of Single
i TITLE OF INVENTION: Mucleotide Polymorphisms in the Human Genome
i TITLE OF INVENTION: NUMBER: US/09/925,065A
; TITLE OF INVENTION: NUMBER: US/09/925,065A
; CURRENT APPLICATION NUMBER: US 60/243,096
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR PLILNG DATE: 2000-10-24
; PRIOR PLILNG DATE: 2000-11-20
; PRIOR PLILNG DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR PLILNG DATE: 2001-01-16
; PRIOR FILING DATE: 2001-01-16
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Pred. No. 6.6;
0; Mismatches
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l Similarity 53.1%;
78; Conservative (
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; ORGANISM: Homo sapiens
US-09-925-065A-147413
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Best Local Similarity
477
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                                                  Sequence 209, Application US/11117187

Publication No. US20050266560A1

GENERAL INFORMATION:
APPLICANT: PREUS. DAPHNE

APPLICANT: COPENHAVER, GREGORY

TITLE OF INVENTION: PLANT ARTIFICIAL CHROMOSOME COMPOSITIONS AND METHODS
FILE REPERRING: ARCD:309US
CURRENT APPLICATION NUMBER: US/11/117,187

CURRENT APPLICATION NUMBER: US/09/531,120

PRIOR FILING DATE: 2000-03-17

PRIOR FILING DATE: 1999-03-18

NUMBER OF SEQ ID NOS: 212

SOFTWARE: PATENT VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL VERIL V
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      199 GCCGCTCGCACACTCGAAGACTTTAAAGCTGCTTATAAAGGGTGGCAGCTCATCGATCAG 258
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GENERAL INFURCATION:

TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT APPLICATION NUMBER: US 60/243,096
PRIOR PRILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR PILING DATE: 2000-11-30
PRIOR PILING DATE: 2001-01-16
PRIOR PILING DATE: 2001-01-16
PRIOR PILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-05-09
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FRAESEQ for Windows Version 4.0
LENGTH: 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 611587;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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Best Local Similarity 51.9%; Pred. No. 96;
Matches 83; Conservative 0; Mismatches 77;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Arabidopsis thaliana US-11-117-187-209
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Matches 93; Conservative
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                                 US-11-117-187-209/c
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Sequence 47253, Application US/09925065A
Sequence 47253, Application US/09925065A
Sublication No. US20040181048A1
SEREMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: UNCLEOCIDE POLYMORPHISMS in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US 60/255,065A
CURRENT FILING DATE: 2000-10-24
PRIOR FILING DATE: 2000-11-20
PRIOR FILING DATE: 2000-11-20
PRIOR FILING DATE: 2000-11-30
PRIOR PILING DATE: 2001-01-16
PRIOR PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
PRIOR PRIOR DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
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Pred. No. 7.5;
0; Mismatches 86; Indels
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR PELING DATE: 2000-11-30
PRIOR FILING DATE: 2000-11-30
PRIOR FILING DATE: 2001-11-16
PRIOR RILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-05
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FABLESEQ for Windows Version 4.0
SCATUL SEQ ID NOS: 957086
LENGTH: 580
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Best Local Similarity 50.6%;
Matches 88; Conservative 0
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US-09-925-065A-477253
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US-09-925-065A-720480
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US-09-925-065A-477253/c
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LENGTH: 581
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APPLICANT: CIBELLI, JOSE
APPLICANT: CIBELLI, JOSE
APPLICANT: CORDAD DE MEGALHAES, GUILHERME
APPLICANT: O'ORDAD DE MEGALHAES, GUILHERME
APPLICANT: CROSBY, JAVIER A.
TITLE OF INVENTION: CORRELATES TO FERTILITY, OVARIAN FUNCTION AND/OR FETAL/NEWBORN
TITLE OF INVENTION: VIABILITY
FILE REFERENCE: 53942US
CURRENT APPLICATION NUMBER: 1201/091,883
CURRENT FILING DATE: 2005-03-29
PRIOR APPLICATION NUMBER: 60/556,875
PRIOR APPLICATION NUMBER: 60/556,875
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Pred. No. 13;
0; Mismatches 106;
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Job time : 942 secs
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              Sequence 216, Application US/11091883
Publication No. US20060024693A1
GENERAL INFORMATION:
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Best Local Similarity 48.5%;
Matches 100; Conservative
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US-11-091-883-216
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SEQ ID NO 216
LENGTH: 2279
US-11-091-883-216
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Sequence 22, Appl
Sequence 2228, Ap
Sequence 361, Appl
Sequence 960, Appl
Sequence 1, Appli
Sequence 1, Appli
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Sequence 2141, Ap
Sequence 12467, A
Sequence 16275, A
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2142, Ap
3189, Ap
6958, Ap
555, App
22, Appl
2228, Ap
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Sequence 13007, A
Sequence 12464, A
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Sequence 2478, Ap
                                               06:32:16 ; Search time 233 Seconds (without alignments) 8048.616 Million cell updates/sec
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Biocceleration Ltd.
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US-09-252-991A-12464
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US-08-781-986A-302
US-09-107-433-1114
US-09-583-110-2142
US-09-583-110-2142
US-09-583-110-2142
US-09-584-0002-3189
US-09-586-002-22
US-09-596-002-22
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US-09-949-016-12467
US-09-949-016-16275
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version - 2006 H
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Maximum Match 100%
Listing first 45 summaries
                               - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
GenCore (c) 1993
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                                                 February 27, 2006,
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seq length: 200000000
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Sequence 780, Application US/09134001C

Sequence 780, Application US/09134001C

Patent No. 6380370

BARERAL INFORMATION:
APPLICANT: LYAN DOUGETE-Stamm et al
TITLE OF INVENTION: BEIDERMIDIS FOR DIAGNOSTICS AND THERABEUTICS

TITLE OF INVENTION: BEIDERMIDIS FOR DIAGNOSTICS AND THERABEUTICS

FILE REFERENCE: GTC-007

CURRENT APPLICATION NUMBER: US/09/134,001C

CURRENT FILING DATE: 1998-08-13

PRIOR PAPLICATION NUMBER: US 60/064,964

PRIOR FILING DATE: 1997-11-08

PRIOR PELING DATE: 1997-11-08

PRIOR PELING DATE: 1997-08-14

NUMBER OF SEQ ID NOS: 5674

SEQ ID NO.780

LENGTH: 615
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            912
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74 cardrodcaraddriarcaaacacccraarrocrarcgrirroaaaararcrrg 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAAAAGAAGTCCAAATTTATACTTCACTAATTGTACGAGAAGATGCTCAACTACTATATG 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCCCAAAAGGAGCGCTTGCGATCCTCGCTTCCGGCGATCCGGGGAGCGGTGATTGAAGCGA 972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    739 ACGGCGGGATCGGCTATCAGATCTTCACGCCAAATCCGTTTATTATAAGAAAAACAGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCTTTTCGACAAGGAAGAAAAATGCTGTTTACGAAAATGCTGAATGTTACGGGGGTTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14 retargearatarakagaacarrarcreagricricecracacargiagigerreaga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCTTTATTAATGAAGGAAAAGAAATGTTTCTTAGCTTAATAAAGTGACTGGGATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAGAAACAATC----TATACATACCATTATGTAAGAGAGACACGAATGCGCTGTACG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9.8%; Score 103.4; DB 3; Length 56.4%; Pred. No. 3.8e-23; ive 0; Mismatches 161; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: DNA; CRGANISM: Staphylococcus epidermidis US-09-134-001C-780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 9.8
Best Local Similarity 56.4
Matches 216; Conservative
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us-10-510-408-1.rni

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Gil H. Choi
Patrick S. Dillon
Craig A. Rosen
Steven C. Barash
Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
                                                                          11648 GCCATTGAAACCAAGAACATCACCTACTTGACCAAGTTCCCTAAAATTGGCAAGAAAAA 11707
                             969 GCGATCGAGAATGAGGACGAAGCATTTCTCGTCAAATTTCCCGGCGTAGGCAAAAAAAGG 1028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3226 reracecerarercaaaceraaerraacacarrrarareceraecaceraeracirerreaaa 3285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3286 CIGCIGGIGITIGGATITCAACACCAAATITCITATCGTITTCAAAAGCATCTAG 3345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         793 ACAGCAAAGAAACAATCTATACATACCATTATGTAAGAGAAGACACGAATGCGCTGTACG 852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      739 ACGCCGCGATCGCTATCACGCCAAATCCGTTTATTAAGAA-----AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  679 IGATCGAATTCGTAAAAGGGACGATTGATTATGTATCGCCCCCAATATATTGTCATTGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORPUTER: REACALLE FORM:

COMPUTER: He Vectra 486/33

COMPUTER: HP Vectra 486/33

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/956,171E

FILING DATE: 20-0ct-1997

CLASSIFICATION: cUnknown>
PRIOR APPLICATION: CORPUTER: 09/09/861

FILING DATE: January 5, 1996

APPLICATION NUMBER: 09/181,986

FILING DATE: January 3, 1997

ATTORNEY/AGENT INFORMATION:
NAME: MACH AND NUMBER: 46,789

REFERENCE/DOCKET NUMBER: 46,789

REFERENCE/DOCKET NUMBER: 46,789

TELECOMONICATION NUMBER: 46,789

TELECOMONICATION NUMBER: 46,789

TELECOMONICATION NUMBER: 46,789

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TELECOMONICATION NUMBER: 46,789
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Pred. No. 9.1e-18;
0; Mismatches 170; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
                                                                                                                                                                                 11708 GCCCAGCAGATGGTGCTGGACTTGGAA 11734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 302:
                                                                                                                                 1029 GCAAGGCAGATCATCCTTGACCTGAAA
                                                                                                                                                                                                                                                                                                         Sequence 302, Application US/08956171E Patent No. 659314
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (301) 309-8.
INFORMATION FOR SEQ ID NO: 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 54.0%;
Matches 207; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS
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COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: Maryland COUNTRY: USA
                                                                                                                                                                                                                                                         RESULT 3
US-08-956-171E-302
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                                                                                                                                                                                                                                      Sequence 40, Application US/08961527
Patent No. 6420135
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
NUMBER OF SEQUENCES: 391
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11588 ATTGGTCCTGTATCAGCTCTTGCTATTATCGCTGCTGATGACAATGCTGGCTTGGTTCAA 11647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11348 ACTATGTACGCATATTTAAAAGGAATCATTACCAAAATTACTGCCAAATACATTGTTCTT 11407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  788
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11408 GAAACCAATGGTATTGGTTATATCCTGCATGTGGCCAATCCTTATGCCTATTCAGGTCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11468 GTTAATCAGGAGGCTCAGATTTAIGTGCATCAGGTIGTGCGTGAGGACGCCCATTTGCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         909 ATCGGCCCAAAAGGAGCGCTTGCGATCCTCGGCGATCCGGCGAGCGGTGATTGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              675 ACGTTGATCGAATTCGTAAAAGGGACGATTGATTATGTATCGCCCCAATATATTGTCATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  735 GAAAACGGCGGGATCGGCTAT----CAGATCTTCACGCCAAATCCGTTTATTATAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  789 AAAAACAGCAAAGAAACAATCTATACATACCATTATGTAAGAGAAGACACGAATGCGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       849 TACGGCTTTTCGACAAGGGAAGAAAAATGCTGTTTACGAAAATGCTGAATGTTACGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11528 raridicariricecricagasicaricas and contrinental controcerences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 89.8; DB 3; Length 1.
Pred. No. 7.6e-18;
0; Mismatches 172; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33 OPERATING SYSTEM: MSDOS version 6.2
                                                                                                                                                                                                                                                                                                                                                        STREET: 9410 Key West Avenue STATE: Maryland COUNTRY: Irea ZIP.
                                                                               1033 GCCAGATCATCCTTGACCTGAAA 1055
                                                                                                                            374 GACAAATTGTGTTAGATTTAAAA 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Brookes, A. Anders
REGISTRATION UNDBER: 36,373
REFRENCE/DOCKET NUMBER: PB34(
TELEPHONE: (301) 309-8504
TELEPHONE: (301) 309-8512
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 54.0%;
Matches 209; Conservative
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TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
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793 ACAGCAAAGAAACAATCTATACATACCATTATGTAAGAGAAGACACGAATGCGCTGTACG
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ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
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CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/09/107,433
    FILING DATE: 30-Jun-1998
    PRIOR APPLICATION DATA:
    APPLICATION NUMBER: 60/085131
    PILING DATE: May 12, 1998
    APPLICATION NUMBER: 60/051553
    PILING DATE: JULY 2, 1997
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1033 GGCAGATCATCCTTGACCTGAAA 1055
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: «Unknown»
OPERATING SYSTEM: «Unknown»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1114, Application US/09107433
Patent No. 6800744
GENERAL INFORMATION:
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MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 609 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 1114:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 5206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 02354
COMPUTER READABLE FORM:
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US-09-107-433-1114
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3346 ATCATGAAGTTTTAATTCATACATCTTTAATTGTTCGTGAAGATGCACAATTATTGTATG 3405
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APPLICANT: Charles Kunsch
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
                                                                                                           GCTTTTCGACAAGGAAGAAAAAATGCTGTTTACGAAAATGCTGAATGTTACGGGGATCG
                                                                                                                                                                                                                                                                                                                                                                                        TCGAGAATGAGGACGAAGCATTTCTCGTCAAATTTCCCGGCGTAGGCAAAAAACGGCAA
                                                                                                                                                                        GCCCAAAAGGAGCGCTTGCGATCCTCCGCCGATCCGGGAGCGGTGATTGAAGCGA
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Pred. No. 9.1e-18;
0; Mismatches 170; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue CITY: Rockville STATE: Maryland COUNTRY: USA
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
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Patent No. 6737248
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB246
TELECOMMUNICATION INFORMATION:
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TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 302:
SEQUENCE CHRACTERISTICS:
LENGTH: 7159 base pairs
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Matches 207; Conservative C
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US-08-781-986A-302
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US-08-781-986A-302
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FOR DIAGNO 3526 TIGAAAATGAAAATGATACGTATTTAACTAAATTCCCAGGAATTGGTAAGAAAACGGCAA 3585 3346 ATCATGAAGTTTTAATTCATACATCTTTAATTGTTCGTGAAGATGCACAATTATTGTATG 3405 3466 GTCCGAAATCAGCTTTAGCTATTTTAGCGACAAGTACGCCTAATGAAGTAAAACGTGCCA 3525 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE
THERAPEUTICS 913 GCCCAAAAGGAGCGCTTGCGATCCTCGCTTCCGGCGATCCGGGAGCGGTGATTGAAGCGA 853 GCTTTTCGACAAGGGAAGAAAAATGCTGTTTACGAAAATGCTGAATGTTACGGGGATCG

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sequence 3189, Application US/09134000C

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ATCAGGAGGCTCAGATTTATGTGCATCAGGTTGTGCGTGAGGAGGCCCCATTTGCTTTATG 181
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                                                                                                                                                                                              182 GATTICGCTCAGAGGATGAGAAAAAGCTCTTTCTTAGTCTAATTICGGTCTCTGGGATTG
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Sequence 2142, Application US/09583110

Sequence 2142, Application US/09583110

GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
FILE REFERENCE: PATHOO-07A
CURRENT FILING DATE: 2000-05-26
PRIOR PILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US 60/085,131
PRIOR FILING DATE: 1998-05-12
PRIOR FILING DATE: 1998-05-12

WRING FILING DATE: 1998-05-12

WHING FILING DATE: 1997-07-02

WHENCE FILING DATE: 1997-07-05

WHENCE FILING DATE: 1997-07-05

WHENCE FILING DATE: 1997-07-05

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                                                                                                                                                                                                                                                                                                                                                     13 ACTATGTACGCATATTTAAAAGGAATCATTACCAAAATTACTGCCAAATACATTGTTCTT 72
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                                                                                                                           Length 609;
                                                                                                                   Score 88.2; DB 3; Length 6
Pred. No. 3.6e-18;
0; Mismatches 173; Indele
       DESCRIPTION: SEQ ID NO: 1114:
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US-09-583-110-2142
                                                                                                                   8.4%;
ilarity 53.7%;
Conservative
                                                                                                                                                          Similarity
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US-09-583-110-2142
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US-09-107-433-1114
                                                                                                                                                          Best Local Simi
Matches 208;
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Best Local S:
Matches 206
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APPLICANT: Berg, Kim, L.
APPLICANT: Berg, Kim, L.
APPLICANT: Berg, Kim, L.
APPLICANT: Berg, Kim, L.
APPLICANT: Berg, Kim, L.
APPLICANT: Berg, Kim, L.
APPLICANTION: NUCHBER: US/09/596,002
CURRENT APPLICATION NUMBER: 1000-06-16
PRIOR APPLICATION NUMBER: 60/140,121
PRIOR PILING DATE: 1999-06-18
PRIOR PILING DATE: 1999-06-18
PRIOR PILING DATE: 1999-06-18
209 ATGATCGTGATATTTTTAGAAAGCTGATCAAAATTAACGGCGTAGGTGCTAAAAATGGCGT
                                                                                                                                   269 TAGCAATGCTTTCAACCCTAAGCGTTGCCGAGATTAAACACGCTATTGAAACAGATTATG
                                                                                                                                                                                      TCTATACATACCATTATGTAAGAGAAGACACGAATGCGCTGTACGGCTTTTCGACAAGGG
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53.0%; Pred. No. 3.2e-08;
ive 0; Mismatches 116; Indels
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; OTHER INFORMATION: Incyte template ID No. 6632636
; PUBLICATION INFORMATION:
US-09-596-002-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 22, Application US/09596002
; Patent No. 6632636
GENERAL INFORMATION:
; APPLICANT: Lagace, Robert, E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PERL Program
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ORGANISM: M. catarrhalis
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US-09-328-352-2228
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US-09-540-236-555
US-09-540-236-555
Sequence 555, Application US/09540236
Patent No. 6673310
GENERAL INFORMATION:
APPLICANT: GATY L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/540,236
CURRENT PILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 3840
SEQ ID NO 555
LENGTH: 624
                                                                 Sequence 6958, Application US/09489039A
Patent No. 6610836
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
TITLE OF INVENTION: NUMBER: US/09/489,039A
CURRENT APPLICATION NUMBER: US 60/117,747
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 6958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              988 AAGCATTTCTCGTCAAATTTCCCGGCGTAGGCAAAAAAAGGCAAGGCAGATCATCCTTG 1047
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  161 TCTTCACCCACTTTGTGGTGCGTGAAGATGCCCAGCTGCTGTATGGGTTTAACAAAAC 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            341 TCGCCTCGCTGGTGAAGCTGCCGGGGATTGGCAAAAAAACCGCTGAGCGTCTGATCGTTG 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            808 TCTATACATACCATTATGTAAGAGAAGACACGAATGCGCTGTACGGCTTTTCGACAAGGG 867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     221 AGGAACGTACCCTGTTTAAAGAGCTGATTAAAACCAACGGCGTGGGGCCCAAGCTGGCGC 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         868 AAGAAAAAATGCTGTTTACGAAAATGCTGAATGTTACGGGGATCGGCCCCAAAAGGAGCGC 927
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5.8%; Score 61.4; DB 3; Length 624;
53.0%; Pred. No. 2.3e-09;
iive 0; Mismatches 116; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Klebsiella pneumoniae
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Matches 131; Conservative
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US-09-540-236-555
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                                                 US-09-489-039A-6958
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987 GAAGCATTTCTCGTCAAATTTCCCGGCGTAGGCAAAAAAAGGGCAAGGCAGATCATCCTT 1046
                                                                         18-09-221-017B-960/c
| Sequence 960, Application US/09221017B
| Patent No. 6444799
| Patent No. 6444790|
| APPLICANT: ROSS, Bruce C. APPLICANT: ROSS, Bruce C. APPLICANT: ROSS, Bruce C. APPLICANT: ROSS, Bruce C. APPLICANT: ROSS, Bruce C. APPLICANT: ROSS, 1120
| CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: AD
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ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IEM COMPATION
OFFERATING SYSTEM: Windows
SOFTWARE: FEALSEQ for Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/221,017B
FILING DATE: 23-DEC-1998
CLASSIFICATION NUMBER: PP1182
FILING DATE: 31-DEC-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP146
FILING DATE: 30-JAN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP194
FILING DATE: 09-APR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP2911
FILING DATE: 10-DEC-1998
FILING DATE: 10-DEC-1998
ATTORNEY, AGENT IN FORMATION:
ATTORNEY, AGENT IN FORMATION:
ATTORNEY, AGENT IN FORMATION:
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4.8%; Score 50.6; DB 3;
Best Local Similarity 49.1%; Pred. No. 2.2e-05;
Matches 134; Conservative 0; Mismatches 139;
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REGISTRATION NUMBER: 32,430
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-434-0792
TELEFAX: 650-444-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: DNA (genomic)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
LOCATION: 1...3250
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STRANDEDNESS: double
                                                                                                                                              1047 GACCTGAAA 1055
                                                                                                                                                                                                                415 GAAATGAAA 423
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ANTI-SENSE: U
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                                                                                                                                                                                                                                                                                                                      RESULT 13
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Patent No. 6605709
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR PILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NOS: 8344
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                235 CAAGAACGGGCATTGTTTCGTGAATTGATAAAAGTCAATGGTGTAGGGCCTAAGCTAGCA 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      927 CTTGCGATCCTCGCTTCCGGCGATCCGGGAGCGGTGATTGAAGCGATCGAGAATGAGGAC 986
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               185 TTTATGGTTTTAGGATGCTCAAGAAAACTATTTCCGCACCTTACTAAAAGTAAATG 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     907 GGATCGGCCCAAAAGGAGCGCTTGCGATCCTCGCTTCCGGCGATCCGGGAGCGGTGATTG 966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          245 GTGTGGGCCCGAAAATGGCATTAGGTATTCTTCTACGTTAAGTGTTGAATTGCTGGTAC 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          305 ACACAATTGAACATGACGATGTGAATACTTTGGTTAAAGTTCCGGGTGTAGGCAAAAAA 364
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Pred. No. 5.8e-09;
0; Mismatches 118; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                Length 609;
                                                                                                                                                                                                                                                                                                                                                                                                                        Score 60.2; DB 3; Length 6
Pred. No. 5.5e-09;
0; Mismatches 128; Indels
                                                                 FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 2228
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                                                                                                                                                                                                                                                                                     ; TYPE: DNA
; ORGANISM: Acinetobacter baumannii
US-09-328-352-2228
                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 5.7%;
Best Local Similarity 51.7%;
Matches 137; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 52.6%;
Matches 131; Conservative (
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CRGANISM: Proteus mirabilis
US-09-543-681A-361
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344775 GAGAAGATTTCTAAACTTACTAAAATTCCAGGTGTTGGCAAAAAACAGCTGAACGTT 344716
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4.6%; Score 49; DB 3; Length 183
Best Local Similarity 49.4%; Pred. No. 0.0036;
Matches 127; Conservative 0; Mismatches 130; Indels
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Hamilton O. Smith
J. Craig Venter
J. Craig Tenter
TITLE OF INVENTION: The Mucleotide sequence of
the Haemophilus influenzae
Thereof, and Uses Thereof
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ADDRESSE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville,
STATE: MD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/643,990A
FILING DATE: 23-Aug-2000
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/487,429
FILING DATE: 1995-06-07
APPLICATION NUMBER: 08/426,787
APPLICATION NUMBER: 08/426,787
ATTORNEY/AGENT: INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Kenley K. Hoover
REGIGTRATION NUMBER: 40,302
REFERENCE/DOCKET NUMBER: PB186F1C1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: 3 1/2 inch diskette
COMPUTER: Dell Pentium
OPERATING SYSTEM: MS DOS v6.22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Robert D. Fleischmann
Mark D. Adams
                                                                                                                                                                                                                                                                                                                                                                 344715 rgrragirgagcrcaaa 344699
                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-643-990A-1/c; Sequence 1, Application US/09643990A; Patent No. 6528289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: 301-610-5790
TELEFAX: 310-309-8439
                                                                                                                                                                                                                                                                                                                 TCATCCTTGACCTGAAA 1055
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                                                                                                                                                                                                                                                                                      963 ATTGAAGCGATCGAGAATGAGGACGAAGCATTTCTCGTCAAATTTCCCGGCGTAGGCAAA 1022
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                                            1540 raticalgegalagalagagagagagartaringartagagagargarogagagargoccar 1481
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783 TATAAGAAAAACAGCAAAGAAACAATCTATACATACCATTATGTAAGAGAAGACACGAAT 842
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Sequence 1, Application US/09557884
Patent No. 6506581
GENERAL INPORMATION:
APPLICANT: Fleischmann et al.
TITLE OF INVENTION: The Nucleotide sequence of
TITLE OF TAVENTION: The Haemophilus influenzae Rd Genome, Fragments
Thereof, and Uses Thereof
                                                                                              843 GCGCTGTACGGCTTTTCGACAAGGAAAAAAATGCTGTTTACGAAAAATGCTGAATGTT
                                                                                                                                                                                          903 ACGGGGATCGGCCCAAAAGGAGCGCTTGCGATCCTCGCTTCCGGCGGTGCCGGGGGCGGTG
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Pred. No. 0.0036;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: 3 1/2 inch diskette
COMPUTER: Dell Pentium
OPERATING SYSTEM: MS DOS v6.22
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/557,884
FILING DATE: 25-Apr-2000
CLASSIFICATION: «UNHOWN»
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/476,102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: JUN-5-1995
ATTORNEY/AGENT INFORMATION:
NAME: Michelle S. Marke
REGISTRATION NUMBER: 41,971
REFERENCE/DOCKET NUMBER: PB186P3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
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TELEPROME: 301-309-8604
TELEPRAK: 301-309-8439
INFORMATION FOR SEQ ID NO: 1:
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STRANDEDNESS: double
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Matches 127; Conservative
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US-09-557-884-1/c
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Search completed: February 27, 2006, 06:36:34
Job time : 245 secs
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